

IM-5  
SEQUENCE LISTING

<110> Wonderling, Ramani S.  
Boroughs, Karen L.

<120> CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

<130> IM-5

<140> not yet assigned

<141> 2001-07-27

<150> 60/223,016

<151> 2000-08-04

<160> 109

<170> PatentIn version 3.1

<210> 1

<211> 514

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (114)..(512)

<223>

<220>

<221> misc\_feature

<222> (470)..(470)

<223> n = unknown at position 470  
Xaa = unknown at position 119

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aaaccttcca gatcccttcc tctcttagga aactattgag cacagggata aag atg 116  
Met  
1

act gct ata cca gta gat gat tgc atc aac ttt gtg gga atg aaa ttt 164  
Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys Phe  
5 10 15

att gac aat aca ctt tac ttt gta gct gac agt gat gaa aac ctg gaa 212  
Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu Glu  
20 25 30

aca gat tac ttt ggc aag ctt gaa cat aaa ctc tca atc tta cga aac 260  
Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn  
35 40 45

ttg aac gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt 308  
Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe  
50 55 60 65

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gag gat atg cct gat tct gac tgt aca gat aat gca ccc cgg act gaa 356  
 Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu  
                     70                    75                    80

ttt atc ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta 404  
 Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val  
                     85                    90                    95

acc atc tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac 452  
 Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn  
                     100                    105                    110

aaa att att tcc ttt aan gga atg agt cct cct gag agt atc aat gat 500  
 Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn Asp  
                     115                    120                    125

gaa gga aat gac at 514  
 Glu Gly Asn Asp  
 130

<210> 2  
 <211> 133  
 <212> PRT  
 <213> Felis catus

<220>  
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 <222> (119)..(119)  
 <223> The 'Xaa' at location 119 stands for Lys, or Asn.

<220>  
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 <222> (470)..(470)  
 <223> n = unknown at position 470  
       Xaa = unknown at position 119

<400> 2

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Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu  
                     20                    25                    30

Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg  
                     35                    40                    45

Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val  
                     50                    55                    60

Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr  
 65                    70                    75                    80

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Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala  
85 90 95

Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu  
100 105 110

Asn Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn  
115 120 125

Asp Glu Gly Asn Asp  
130

<210> 3  
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<212> DNA  
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<220>  
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<222> (45)..(45)  
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cctctagtga ggctatcttt atacatatat atgataaatt cagtccgggg tgcattatct 180  
gtacagtcag aatcaggcat atcctcaaac acaggttgat ctccctgggt aatgaagaga 240  
acttgggtcgt tcaagtttcg taagattgag agtttatggt caagcttgcc aaagtaatct 300  
gtttccaggt tttcatcact gtcagctaca aagtaaagtg tattgtcaat aaatttcatt 360  
cccacaaagt tgatgcaatc atctactggg atagcagtca tctttatccc tgtgctcaat 420  
agtttcctaa gagaggaagg gatctggaag gtttgagggt cctttctttt cctgagctgt 480  
gtagatggca gaaggtggca ggagcgcctt tagc 514

<210> 4  
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<212> DNA  
<213> Felis catus

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<222> (3)..(464)  
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<220>  
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 <222> (126)..(126)  
 <223> n = unknown at position 126  
 Xaa = unknown at position 43

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 Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln  
 1 5 10 15  
 gtt ctc ttc att aac cag gga gat caa cct gtg ttt gag gat atg cct 95  
 Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro  
 20 25 30  
 gat tct gac tgt aca gat aat gca ccc cgg nct gaa ttt atc ata tat 143  
 Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr  
 35 40 45  
 atg tat aaa gat agc ctc act aga ggt ctg gca gta acc atc tct gtg 191  
 Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val  
 50 55 60  
 aat tat aag acc atg tct act ctc tcc tgt gag aac aaa att att tcc 239  
 Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser  
 65 70 75  
 ttt aag gaa atg agt cct cct gag agt atc aat gat gaa gga aat gac 287  
 Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp  
 80 85 90 95  
 atc ata ttc ttt cag aga agt gtt cca gga cat gat gat aag ata caa 335  
 Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln  
 100 105 110  
 ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa aaa gag 383  
 Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu  
 115 120 125  
 aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat ggg gat 431  
 Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp  
 130 135 140  
 aag tcc ata atg ttc act gtt caa aac aag aat tagatattaa aattgcataa 484  
 Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn  
 145 150  
 tttgaaaaaa aaaaaaaa 502

<210> 5  
 <211> 154  
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 <213> Felis catus

<220>  
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 <222> (42)..(42)

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<223> The 'Xaa' at location 42 stands for Thr, Ala, Pro, or Ser.

<220>

<221> misc\_feature

<222> (126)..(126)

<223> n = unknown at position 126

Xaa = unknown at position 43

<400> 5

Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val  
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Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp  
20 25 30

Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr Met  
35 40 45

Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn  
50 55 60

Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe  
65 70 75 80

Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile  
85 90 95

Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe  
100 105 110

Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys  
115 120 125

Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys  
130 135 140

Ser Ile Met Phe Thr Val Gln Asn Lys Asn  
145 150

<210> 6

<211> 502

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<213> Felis catus

<220>

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<222> (377)..(377)

<223> n = unknown at position 377

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tctttttcac aagctagaaa gtaccctctg tacaatgaag actcaaattg tatcttatca      180
tcatgtcctg gaacacttct ctgaaagaat atgatgtcat ttccttcac attgatactc      240
tcaggaggac tcatttcctt aaaggaaata attttgttct cacaggagag agtagacatg      300
gtcttataat tcacagagat gggtactgcc agacctctag tgaggctatc tttatacata      360
tatatgataa attcagnccg ggggtgcatta tctgtacagt cagaatcagg catatcctca      420
aacacagggt gatctccctg gttaatgaag agaacttggt cgttcaagtt tcgtaagatt      480
gagagtttat gttcaagctt gc                                          502

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<210> 7
<211> 607
<212> DNA
<213> Felis catus

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<220>
<221> CDS
<222> (24)..(599)
<223>

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<400> 7
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                        1           5           10

aac ttt gtg gga atg aaa ttt att gac aat aca ctt tac ttt gta gct      101
Asn Phe Val Gly Met Lys Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala
                        15           20           25

gac agt gat gaa aac ctg gaa aca gat tac ttt ggc aag ctt gaa cat      149
Asp Ser Asp Glu Asn Leu Glu Thr Asp Tyr Phe Gly Lys Leu Glu His
                        30           35           40

aaa ctc tca atc tta cga aac ttg aac gac caa gtt ctc ttc att aac      197
Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asn
                        45           50           55

cag gga gat caa cct gtg ttt gag gat atg cct gat tct gac tgt aca      245
Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp Ser Asp Cys Thr
                        60           65           70

gat aat gca ccc cgg act gaa ttt atc ata tat atg tat aaa gat agc      293
Asp Asn Ala Pro Arg Thr Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser
                        75           80           85           90

ctc act aga ggt ctg gca gta acc atc tct gtg aat tat aag acc atg      341

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Leu	Thr	Arg	Gly	Leu	Ala	Val	Thr	Ile	Ser	Val	Asn	Tyr	Lys	Thr	Met	
			95						100					105		
tct	act	ctc	tcc	tgt	gag	aac	aaa	att	att	tcc	ttt	aag	gaa	atg	agt	389
Ser	Thr	Leu	Ser	Cys	Glu	Asn	Lys	Ile	Ile	Ser	Phe	Lys	Glu	Met	Ser	
			110					115					120			
cct	cct	gag	agt	atc	aat	gat	gaa	gga	aat	gac	atc	ata	ttc	ttt	cag	437
Pro	Pro	Glu	Ser	Ile	Asn	Asp	Glu	Gly	Asn	Asp	Ile	Ile	Phe	Phe	Gln	
			125				130					135				
aga	agt	gtt	cca	gga	cat	gat	gat	aag	ata	caa	ttt	gag	tct	tca	ttg	485
Arg	Ser	Val	Pro	Gly	His	Asp	Asp	Lys	Ile	Gln	Phe	Glu	Ser	Ser	Leu	
	140					145					150					
tac	aag	ggg	tac	ttt	cta	gct	tgt	gaa	aaa	gag	aaa	gat	ctt	ttc	aaa	533
Tyr	Lys	Gly	Tyr	Phe	Leu	Ala	Cys	Glu	Lys	Glu	Lys	Asp	Leu	Phe	Lys	
155					160					165					170	
ctc	att	ttg	aaa	aaa	aag	gat	gaa	aat	ggg	gat	aag	tcc	ata	atg	ttc	581
Leu	Ile	Leu	Lys	Lys	Lys	Asp	Glu	Asn	Gly	Asp	Lys	Ser	Ile	Met	Phe	
				175					180					185		
act	gtt	caa	aac	aag	aat	tagatatt										607
Thr	Val	Gln	Asn	Lys	Asn											
				190												
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			20					25					30			
Glu	Thr	Asp	Tyr	Phe	Gly	Lys	Leu	Glu	His	Lys	Leu	Ser	Ile	Leu	Arg	
		35					40					45				
Asn	Leu	Asn	Asp	Gln	Val	Leu	Phe	Ile	Asn	Gln	Gly	Asp	Gln	Pro	Val	
	50					55					60					
Phe	Glu	Asp	Met	Pro	Asp	Ser	Asp	Cys	Thr	Asp	Asn	Ala	Pro	Arg	Thr	
65					70					75					80	
Glu	Phe	Ile	Ile	Tyr	Met	Tyr	Lys	Asp	Ser	Leu	Thr	Arg	Gly	Leu	Ala	
				85					90					95		

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Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu  
 100 105 110

Asn Lys Ile Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn  
 115 120 125

Asp Glu Gly Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His  
 130 135 140

Asp Asp Lys Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu  
 145 150 155 160

Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys  
 165 170 175

Asp Glu Asn Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn  
 180 185 190

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 <213> Felis catus

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 gaacataaac tctcaatctt acgaaacttg aacgaccaag ttctcttcat taaccaggga 180  
 gatcaacctg tgtttgagga tatgcctgat tctgactgta cagataatgc accccggact 240  
 gaatttatca tatatatgta taaagatagc ctactagag gtctggcagt aaccatctct 300  
 gtgaattata agaccatgtc tactctctcc tgtgagaaca aaattatttc cttaagga 360  
 atgagtcctc ctgagagtat caatgatgaa ggaaatgaca tcatattctt tcagagaagt 420  
 gttccaggac atgatgataa gatacaattt gagtcttcat tgtacaaggg gtactttcta 480  
 gcttgtgaaa aagagaaaga tcttttcaaa ctcatatttga aaaaaaagga tgaaaatggg 540  
 gataagtcca taatgttcac tgttcaaaac aagaat 576

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 <213> Felis catus

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tacaatgaag	actcaaattg	tatcttatca	tcatgtcctg	gaacacttct	ctgaaagaat	180
atgatgtcat	ttccttcatc	attgatactc	tcaggaggac	tcatttcctt	aaaggaaata	240
attttgttct	cacaggagag	agtagacatg	gtcttataat	tcacagagat	ggttactgcc	300
agacctctag	tgaggctatc	tttatacata	tatatgataa	attcagtcctg	gggtgcatta	360
tctgtacagt	cagaatcagg	catatcctca	aacacagggt	gatctccctg	gttaatgaag	420
agaacttggg	cgttcaagtt	tcgtaagatt	gagagtttat	gttcaagctt	gccaaagtaa	480
tctgtttcca	ggttttcatc	actgtcagct	acaaagtaaa	gtgtattgtc	aataaatttc	540
attcccacaa	agttgatgca	atcatctact	ggtatagcag	tcatctttat	ccctgtgctc	600
aatagtt						607

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<220>  
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<222> (1) .. (471)  
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Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu			
115	120	125	
aaa gag aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat			432
Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn			
130	135	140	
ggg gat aag tcc ata atg ttc act gtt caa aac aag aat			471
Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn			
145	150	155	

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<400> 12

Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn
1 5 10 15

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20 25 30

Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu Phe Ile
35 40 45

Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile
50 55 60

Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile
65 70 75 80

Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly
85 90 95

Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys
100 105 110

Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu
115 120 125

Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn
130 135 140

Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn

145

150

155

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 agactcaaat tgtatcttat catcatgtcc tggaacactt ctctgaaaga atatgatgtc 180  
 atttccttca tcattgatac tctcaggagg actcatttcc ttaaaggaaa taattttgtt 240  
 ctcacaggag agagtagaca tgggtcttata attcacagag atgggtactg ccagacctct 300  
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 <213> Felis catus

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 gtc ggc atg ggg acg gtc aac ggc ttg ctg gat gaa ctc ttt gag aaa 96  
 Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys  
 20 25 30  
 aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct 144  
 Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala  
 35 40 45  
 acc gtt atg gac aag gcc cga gct ctg atc gac agc gtc ctg cgg aaa 192  
 Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys  
 50 55 60  
 ggg cca cgg gcg tgc cag atc ttt atc tgt cac atc tgt gag gaa gac 240  
 Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp  
 65 70 75 80  
 acc cac ctt gca gag acg ctg ggg ctc tcc tca agc cca caa tct gga 288

																IM-5	
Thr	His	Leu	Ala	Glu	Thr	Leu	Gly	Leu	Ser	Ser	Ser	Pro	Gln	Ser	Gly		
				85					90					95			
aat	tct	cag	aac	acc	acg	gac	tct	gaa	gta	gcg	ttt	cct	cct	ctt	cca	336	
Asn	Ser	Gln	Asn	Thr	Thr	Asp	Ser	Glu	Val	Ala	Phe	Pro	Pro	Leu	Pro		
				100					105					110			
gcc	agc	gtg	aat	aac	atg	cct	ggg	ccg	gct	gag	cca	gaa	gaa	tct	gta	384	
Ala	Ser	Val	Asn	Asn	Met	Pro	Gly	Pro	Ala	Glu	Pro	Glu	Glu	Ser	Val		
				115					120					125			
gat	gct	ctc	aag	ctt	tgt	cct	cgt	gaa	aac	ttc	gtg	aaa	ctg	tgt	aaa	432	
Asp	Ala	Leu	Lys	Leu	Cys	Pro	Arg	Glu	Asn	Phe	Val	Lys	Leu	Cys	Lys		
				130					135					140			
cag	agg	gct	gaa	gag	atc	tac	cca	ata	aag	gag	aga	aag	gat	cgt	act	480	
Gln	Arg	Ala	Glu	Glu	Ile	Tyr	Pro	Ile	Lys	Glu	Arg	Lys	Asp	Arg	Thr		
145					150					155					160		
cgt	ctg	gct	ctc	atc	ata	tgc	aat	acg	acg	ttc	gat	cat	ctt	tct	ctc	528	
Arg	Leu	Ala	Leu	Ile	Ile	Cys	Asn	Thr	Thr	Phe	Asp	His	Leu	Ser	Leu		
				165					170					175			
agg	aag	ggg	gct	gac	ctt	gac	gtt	gca	ggg	atg	agg	agg	ctg	ctt	aca	576	
Arg	Lys	Gly	Ala	Asp	Leu	Asp	Val	Ala	Gly	Met	Arg	Arg	Leu	Leu	Thr		
				180					185					190			
gac	ctt	ggc	tac	agt	gtg	cac	ata	aaa	gag	gaa	ctc	act	gct	aag	gac	624	
Asp	Leu	Gly	Tyr	Ser	Val	His	Ile	Lys	Glu	Glu	Leu	Thr	Ala	Lys	Asp		
				195					200					205			
atg	gaa	tca	gag	ctg	agg	gca	ttt	gct	gcc	cgt	cca	gag	cac	aag	tcc	672	
Met	Glu	Ser	Glu	Leu	Arg	Ala	Phe	Ala	Ala	Arg	Pro	Glu	His	Lys	Ser		
				210					215					220			
tcg	gac	agc	aca	ttc	ctg	gtg	ttc	atg	tct	cat	ggc	atc	ctg	agt	gga	720	
Ser	Asp	Ser	Thr	Phe	Leu	Val	Phe	Met	Ser	His	Gly	Ile	Leu	Ser	Gly		
225					230					235					240		
atc	tgt	ggg	acg	aag	tac	agc	gct	gaa	gga	gac	cca	gat	gta	ttg	gct	768	
Ile	Cys	Gly	Thr	Lys	Tyr	Ser	Ala	Glu	Gly	Asp	Pro	Asp	Val	Leu	Ala		
				245					250					255			
tat	gac	acc	atc	ttc	cag	att	ttc	aac	aac	cgc	aac	tgc	ctt	agt	cta	816	
Tyr	Asp	Thr	Ile	Phe	Gln	Ile	Phe	Asn	Asn	Arg	Asn	Cys	Leu	Ser	Leu		
				260					265					270			
aag	gac	aag	ccc	aag	gtc	atc	atc	gtc	cag	gcc	tgc	aga	ggg	gaa	aat	864	
Lys	Asp	Lys	Pro	Lys	Val	Ile	Ile	Val	Gln	Ala	Cys	Arg	Gly	Glu	Asn		
				275					280					285			
ttg	ggg	gaa	ctg	ttg	atc	agt	gac	tct	cca	gcg	gcc	cca	atg	gac	agc	912	
Leu	Gly	Glu	Leu	Leu	Ile	Ser	Asp	Ser	Pro	Ala	Pro	Met	Asp	Ser			
				290					295					300			
act	tca	cag	atg	ggg	agc	agc	ctt	tca	cag	gtg	ggg	gac	aac	cta	gag	960	
Thr	Ser	Gln	Met	Gly	Ser	Ser	Leu	Ser	Gln	Val	Gly	Asp	Asn	Leu	Glu		
305					310					315					320		

IM-5

gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc	1008
Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe	
325 330 335	
tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga	1056
Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly	
340 345 350	
tct ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg	1104
Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp	
355 360 365	
tgc ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa	1152
Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu	
370 375 380	
aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg	1200
Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met	
385 390 395 400	
aca aga tgt ttc tac ctc ttc cca gga cat taa	1233
Thr Arg Cys Phe Tyr Leu Phe Pro Gly His	
405 410	
<210> 15	
<211> 410	
<212> PRT	
<213> Felis catus	
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Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Gln Phe Ile Asn Ser	
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Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys	
20 25 30	
Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala	
35 40 45	
Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys	
50 55 60	
Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp	
65 70 75 80	
Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly	
85 90 95	
Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro	
100 105 110	

## IM-5

Ala	Ser	Val	Asn	Asn	Met	Pro	Gly	Pro	Ala	Glu	Pro	Glu	Glu	Ser	Val	115	120	125
Asp	Ala	Leu	Lys	Leu	Cys	Pro	Arg	Glu	Asn	Phe	Val	Lys	Leu	Cys	Lys	130	135	140
Gln	Arg	Ala	Glu	Glu	Ile	Tyr	Pro	Ile	Lys	Glu	Arg	Lys	Asp	Arg	Thr	145	150	155
Arg	Leu	Ala	Leu	Ile	Ile	Cys	Asn	Thr	Thr	Phe	Asp	His	Leu	Ser	Leu	165	170	175
Arg	Lys	Gly	Ala	Asp	Leu	Asp	Val	Ala	Gly	Met	Arg	Arg	Leu	Leu	Thr	180	185	190
Asp	Leu	Gly	Tyr	Ser	Val	His	Ile	Lys	Glu	Glu	Leu	Thr	Ala	Lys	Asp	195	200	205
Met	Glu	Ser	Glu	Leu	Arg	Ala	Phe	Ala	Ala	Arg	Pro	Glu	His	Lys	Ser	210	215	220
Ser	Asp	Ser	Thr	Phe	Leu	Val	Phe	Met	Ser	His	Gly	Ile	Leu	Ser	Gly	225	230	235
Ile	Cys	Gly	Thr	Lys	Tyr	Ser	Ala	Glu	Gly	Asp	Pro	Asp	Val	Leu	Ala	245	250	255
Tyr	Asp	Thr	Ile	Phe	Gln	Ile	Phe	Asn	Asn	Arg	Asn	Cys	Leu	Ser	Leu	260	265	270
Lys	Asp	Lys	Pro	Lys	Val	Ile	Ile	Val	Gln	Ala	Cys	Arg	Gly	Glu	Asn	275	280	285
Leu	Gly	Glu	Leu	Leu	Ile	Ser	Asp	Ser	Pro	Ala	Ala	Pro	Met	Asp	Ser	290	295	300
Thr	Ser	Gln	Met	Gly	Ser	Ser	Leu	Ser	Gln	Val	Gly	Asp	Asn	Leu	Glu	305	310	315
Asp	Asp	Ala	Ile	Tyr	Lys	Val	His	Val	Glu	Lys	Asp	Phe	Ile	Ala	Phe	325	330	335
Cys	Ser	Ser	Thr	Pro	His	His	Val	Ser	Trp	Arg	Asp	Val	Asn	Lys	Gly	340	345	350

Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp  
 355 360 365

Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu  
 370 375 380

Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met  
 385 390 395 400

Thr Arg Cys Phe Tyr Leu Phe Pro Gly His  
 405 410

<210> 16  
 <211> 1233  
 <212> DNA  
 <213> Felis catus

<400> 16  
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 ctgggctcta acatttggtt tttcaaatga ctgttgtagc ttccgaaata cttcctccag 120  
 atgaaagcac cacgaatact tttggaagca cgtgatgagt tgtgtaatga agagagatcc 180  
 cttgttcacg tctctccaag acacatgatg tggggctcag gagcagaaag cgatgaagtc 240  
 cttctccacg tggaccttgt aaatggcgct gtcctctagg ttgtcaccca cctgtgaaag 300  
 gctgctaccc atctgtgaag tgctgtccat tggggccgct ggagagtcac tgatcaacag 360  
 ttccccaaa ttttcacctc tgcaggcctg gacgatgatg accttgggct tgccttttag 420  
 actaaggcag ttgcggttgt tgaaaatctg gaagatgggt tcataagcca atacatctgg 480  
 gtctccttca gcgctgtact tcgtcccaca gattccactc aggatgccat gagacatgaa 540  
 caccaggaat gtgctgtccg aggacttgtg ctctggacgg gcagcaaag cctcagctc 600  
 tgattccatg tccttagcag tgagttcctc ttttatgtgc aactgtagc caaggtctgt 660  
 aagcagcctc ctcacccctg caacgtcaag gtcagcccc ttcttgagag aaagatgatc 720  
 gaacgtcgta ttgcatatga tgagagccag acgagtacga tcctttctct cttttattgg 780  
 gtagatctct tcagccctct gtttacacag tttcacgaag ttttcacgag gacaaagctt 840  
 gagagcatct acagattctt ctggctcagc cggcccaggc atgttattca cgctggctgg 900  
 aagaggagga aacgctactt cagagtccgt ggtgttctga gaatttccag attgtgggct 960  
 tgaggagagc cccagcgtct ctgcaagggt ggtgtcttcc tcacagatgt gacagataaa 1020  
 gatctggcac gcccggtggc ctttccgcag gacgctgtcg atcagagctc gggccttgtc 1080

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cataacggta gcgttttcac attttactct ctccatctcc tcttggttca gcacgttttt 1140
ctcaaagagt tcattccagca agccgttgac cgtcccatg ccgactgagt tgatgaactg 1200
cttctcttctc tctttcagga ccttgctggc cat 1233

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<210> 17
<211> 526
<212> DNA
<213> Felis catus

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<220>
<221> CDS
<222> (18)..(524)
<223>

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<400> 17
ggcagcagca aaaagcc atg gcc gac aag gat ctg aag ggc aag agg aag 50
          Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys
          1          5          10

cag ttc atc aac tca gtc ggc atg ggg acg gtc aac ggc ttg ctg gat 98
Gln Phe Ile Asn Ser Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp
          15          20          25

gaa ctc ttt gag aaa aac gtg ctg aac cag gag gag atg gag aga gta 146
Glu Leu Phe Glu Lys Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val
          30          35          40

aaa tgt gaa aac gct acc gtt atg gac aag gcc cga gct ctg atc gac 194
Lys Cys Glu Asn Ala Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp
          45          50          55

agc gtc ctg cgg aaa ggg cca cgg gcg tgc cag atc ttt atc tgt cac 242
Ser Val Leu Arg Lys Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His
          60          65          70          75

atc tgt gag gaa gac acc cac ctt gca gag acg ctg ggg ctc tcc tca 290
Ile Cys Glu Glu Asp Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser
          80          85          90

agc cca caa tct gga aat tct cag aac acc acg gac tct gaa gta gcg 338
Ser Pro Gln Ser Gly Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala
          95          100          105

ttt cct cct ctt cca gcc agc gtg aat aac atg cct ggg ccg gct gag 386
Phe Pro Pro Leu Pro Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu
          110          115          120

cca gaa gaa tct gta gat gct ctc aag ctt tgt cct cgt gaa aac ttc 434
Pro Glu Glu Ser Val Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe
          125          130          135

gtg aaa ctg tgt aaa cag agg gct gaa gag atc tac cca ata aag gag 482
Val Lys Leu Cys Lys Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu
          140          145          150          155

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aga aag gat cgt act cgt ctg gct ctc atc ata tgc aat acg ac  
 Arg Lys Asp Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Thr  
 160 165

526

<210> 18  
 <211> 169  
 <212> PRT  
 <213> Felis catus

<400> 18

Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser  
 1 5 10 15

Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys  
 20 25 30

Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala  
 35 40 45

Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys  
 50 55 60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp  
 65 70 75 80

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly  
 85 90 95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro  
 100 105 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val  
 115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys  
 130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr  
 145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr  
 165

<210> 19  
 <211> 526

<212> DNA  
 <213> Felis catus

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 atctcttcag ccctctgttt acacagtttc acgaagtttt cagcaggaca aagcttgaga 120  
 gcatctacag attcttctgg ctacagccggc ccaggcatgt tattcacgct ggctggaaga 180  
 ggaggaaacg ctacttcaga gtccgtgggtg ttctgagaat ttccagattg tgggcttgag 240  
 gagagcccca gcgtctctgc aagggtgggtg tcttcctcac agatgtgaca gataaagatc 300  
 tggcacgccc gtggcccttt ccgcaggacg ctgtcgatca gagctcgggc cttgtccata 360  
 acggtagcgt tttcacattt tactctctcc atctcctcct gggtcagcac gtttttctca 420  
 aagagttcat ccagcaagcc gttgaccgtc cccatgccga ctgagttgat gaactgcttc 480  
 ctcttgccct tcagatcctt gtcggccatg gctttttgct cgtgcc 526

<210> 20  
 <211> 500  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (3)..(362)  
 <223>

<220>  
 <221> misc\_feature  
 <222> (473)..(473)  
 <223> n = unknown at position 473

<400> 20  
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 Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser Thr  
 1 5 10 15  
 tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag gac 95  
 Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp  
 20 25 30  
 gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc tgc 143  
 Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys  
 35 40 45  
 tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga tct 191  
 Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser  
 50 55 60  
 ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg tgc 239  
 Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys

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      65              70              75
ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa aaa      287
Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys
80              85              90              95

cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg aca      335
Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr
              100              105              110

aga tac ttc tat ctc ttc cct ggc aat tgaaaatagc aatcatgggc      382
Arg Tyr Phe Tyr Leu Phe Pro Gly Asn
              115              120

agtcacagccc ttcttgacca acttggaataa gtaccttagc tagcacaaca cactcattta      442

acgttttggtta tctcaataaaa aatgaaaaca nctaaaaaaaa aaaaaaaaaa aaaaaaaaaa      500

<210> 21
<211> 120
<212> PRT
<213> Felis catus

<220>
<221> misc_feature
<222> (473)..(473)
<223> n = unknown at position 473

<400> 21

Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser Thr Ser
1              5              10              15

Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp Asp
              20              25              30

Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys Ser
              35              40              45

Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser Leu
50              55              60

Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys Phe
65              70              75              80

His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys Pro
              85              90              95

Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr Arg
              100              105              110

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Tyr Phe Tyr Leu Phe Pro Gly Asn  
 115 120

<210> 22  
 <211> 500  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> misc\_feature  
 <222> (28)..(28)  
 <223> n = unknown at position 28

<400> 22  
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 aatgagtgtg ttgtgctagc taaggtactt ttccaagttg gtcaagaagg gctggactgc 120  
 ccatgattgc tattttcaat tgccagggaa gagatagaag tatcttgtca tggatagtcg 180  
 ttcaatgggtg ggcattctggg ctctaacatt tggttttttca aatgactggt gtaccttccg 240  
 aaatacttcc tccagatgaa agcaccacga atacttttgg aagcacgtga tgagttgtgt 300  
 aatgaagaga gatcccttgt tcacgtctct ccaagacaca tgatgtgggg tcgaggagca 360  
 gaaagcgatg aagtccttct ccacgtggac cttgtaaatg gcgtcgtcct ctaggttgtc 420  
 acccacctgt gaaaggctgc taccatctg tgaagtgtg tccattgggg ccgctggaga 480  
 gtcactgatc aacagttccc 500

<210> 23  
 <211> 1230  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (1)..(1230)  
 <223>

<400> 23  
 atg gcc gac aag gat ctg aag ggc aag agg aag cag ttc atc aac tca 48  
 Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser  
 1 5 10 15  
 gtc ggc atg ggg acg gtc aac ggc ttg ctg gat gaa ctc ttt gag aaa 96  
 Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys  
 20 25 30  
 aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct 144  
 Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala  
 35 40 45

acc Thr	gtt Val	atg Met	gac Asp	aag Lys	gcc Ala	cga Arg	gct Ala	ctg Leu	atc Ile	gac Asp	agc Ser	gtc Val	ctg Leu	cgg Arg	aaa Lys	192
ggg Gly	cca Pro	cgg Arg	gcg Ala	tgc Cys	cag Gln	atc Ile	ttt Phe	atc Ile	tgt Cys	cac His	atc Ile	tgt Cys	gag Glu	gaa Glu	gac Asp	240
acc Thr	cac His	ctt Leu	gca Ala	gag Glu	acg Thr	ctg Leu	ggg Gly	ctc Leu	tcc Ser	tca Ser	agc Ser	cca Pro	caa Gln	tct Ser	gga Gly	288
aat Asn	tct Ser	cag Gln	aac Asn	acc Thr	acg Thr	gac Asp	tct Ser	gaa Glu	gta Val	gcg Ala	ttt Phe	cct Pro	cct Pro	ctt Leu	cca Pro	336
gcc Ala	agc Ser	gtg Val	aat Asn	aac Asn	atg Met	cct Pro	ggg Gly	cgc Pro	gct Ala	gag Glu	cca Pro	gaa Glu	gaa Glu	tct Ser	gta Val	384
gat Asp	gct Ala	ctc Leu	aag Lys	ctt Leu	tgt Cys	cct Pro	cgt Arg	gaa Glu	aac Asn	ttc Phe	gtg Val	aaa Lys	ctg Leu	tgt Cys	aaa Lys	432
cag Gln	agg Arg	gct Ala	gaa Glu	gag Glu	atc Ile	tac Tyr	cca Pro	ata Ile	aag Lys	gag Glu	aga Arg	aag Lys	gat Asp	cgt Arg	act Thr	480
cgt Arg	ctg Leu	gct Ala	ctc Leu	atc Ile	ata Ile	tgc Cys	aat Asn	acg Thr	acg Thr	ttc Phe	gat Asp	cat His	ctt Leu	tct Ser	ctc Leu	528
agg Arg	aag Lys	ggg Gly	gct Ala	gac Asp	ctt Leu	gac Asp	gtt Val	gca Ala	ggg Gly	atg Met	agg Arg	agg Arg	ctg Leu	ctt Leu	aca Thr	576
gac Asp	ctt Leu	ggc Gly	tac Tyr	agt Ser	gtg Val	cac His	ata Ile	aaa Lys	gag Glu	gaa Glu	ctc Leu	act Thr	gct Ala	aag Lys	gac Asp	624
atg Met	gaa Glu	tca Ser	gag Glu	ctg Leu	agg Arg	gca Ala	ttt Phe	gct Ala	gcc Ala	cgt Arg	cca Pro	gag Glu	cac His	aag Lys	tcc Ser	672
tcg Ser	gac Asp	agc Ser	aca Thr	ttc Phe	ctg Leu	gtg Val	ttc Phe	atg Met	tct Ser	cat His	ggc Gly	atc Ile	ctg Leu	agt Ser	gga Gly	720
atc Ile	tgt Cys	ggg Gly	acg Thr	aag Lys	tac Tyr	agc Ser	gct Ala	gaa Glu	gga Gly	gac Asp	cca Pro	gat Asp	gta Val	ttg Leu	gct Ala	768
tat Tyr	gac Asp	acc Thr	atc Ile	ttc Phe	cag Gln	att Ile	ttc Phe	aac Asn	aac Asn	cgc Arg	aac Asn	tgc Cys	ctt Leu	agt Ser	cta Leu	816
aag Lys	gac Asp	aag Lys	ccc Pro	aag Lys	gtc Val	atc Ile	atc Ile	gtc Val	cag Gln	gcc Ala	tgc Cys	aga Arg	ggg Gly	gaa Glu	aat Asn	864

## IM-5

ttg ggg gaa ctg ttg atc agt gac tct cca gcg gcc cca atg gac agc 912  
 Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser  
 290 295 300

act tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag 960  
 Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu  
 305 310 315 320

gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc 1008  
 Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe  
 325 330 335

tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga 1056  
 Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly  
 340 345 350

tct ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg 1104  
 Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp  
 355 360 365

tgc ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa 1152  
 Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu  
 370 375 380

aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg 1200  
 Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met  
 385 390 395 400

aca aga tac ttc tat ctc ttc cct ggc aat 1230  
 Thr Arg Tyr Phe Tyr Leu Phe Pro Gly Asn  
 405 410

<210> 24

<211> 410

<212> PRT

<213> Felis catus

<400> 24

Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser  
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Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys  
 20 25 30

Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala  
 35 40 45

Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys  
 50 55 60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp  
 65 70 75 80

## IM-5

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly  
85 90 95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro  
100 105 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val  
115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys  
130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr  
145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu  
165 170 175

Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr  
180 185 190

Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp  
195 200 205

Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser  
210 215 220

Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly  
225 230 235 240

Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala  
245 250 255

Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu  
260 265 270

Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn  
275 280 285

Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser  
290 295 300

Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu





gattctcttca	gccctctgtt	tacacagttt	cacgaagttt	tcacgaggac	aaagcttgag	840
agcatctaca	gattcttctg	gctcagccgg	cccaggcatt	ttattcacgc	tggctggaag	900
aggaggaaac	gctacttcag	agtcctgtgt	gttctgagaa	tttccagatt	gtgggcttga	960
ggagagcccc	agcgtctctg	caagggtggg	gtcttctctca	cagatgtgac	agataaagat	1020
ctggcacgcc	cgtggccctt	tccgcaggac	gctgtctgatc	agagctcggg	ccttgtccat	1080
aacggtagcg	ttttcacatt	ttactctctc	catctctctcc	tggttcagca	cgtttttctc	1140
aaagagttca	tccagcaagc	cgttgaccgt	ccccatgccg	actgagttga	tgaactgctt	1200
cctcttgccc	ttcagatcct	tgctggccat				1230

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<212>      DNA
<213>      Felis catus

<220>
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Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His																	
1	5					10					15						
cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc aat act cct gaa																	96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu																	
	20				25				30								
gaa gat gac atc acc tgg acc tct gac cag agc agt gaa gtc cta ggc																	144
Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly																	
	35				40				45								
tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gca gat gct ggc																	192
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly																	
	50				55				60								
cag tat acc tgt cat aaa gga ggc gag gtt ctg agc cat tcg ttc ctc																	240
Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu																	
65	70					75					80						
ctg ata cac aaa aag gaa gat gga att tgg tcc act gat atc tta agg																	288
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg																	
	85				90				95								
gaa cag aaa gaa tcc aaa aat aag atc ttt cta aaa tgt gag gca aag																	336
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys																	
	100					105					110						
aat tat tct gga cgt ttc acc tgc tgg tgg ctg acg gca atc agt acc																	384
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr																	

## IM-5

115	120	125	
gat ttg aaa ttc act gtc aaa agc agc aga ggc tcc tct gac ccc caa Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln 130 135 140			432
gag gtg act tgt gga gca gcg aca ctc tca gca gag aag gtc aga gtg Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val 145 150 155 160			480
gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser 165 170 175			528
gcc tgc ccg gct gcc gag gag agc cta ccc att gaa gtc gtg gtg gac Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp 180 185 190			576
gct att cac aag ctc aag tac gaa aac tac acc agc agc ttc ttc atc Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile 195 200 205			624
agg gac atc atc aaa ccg gac cca ccc aag aac ctg caa ctg aag cca Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro 210 215 220			672
tta aaa aat tct cgg cat gtg gaa gtg agc tgg gaa tac cct gac acc Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr 225 230 235 240			720
tgg agc acc cca cat tcc tac ttc tcc tta aca ttt ggc gta cag gtc Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val 245 250 255			768
cag ggc aag aac aac aga gaa aag aaa gac aga ctc tcc gtg gac aag Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys 260 265 270			816
acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln 275 280 285			864
gcc aga gac cgc tac tat agc tca tcc tgg agc aac tgg gca tcc gtg Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val 290 295 300			912
tcc tgc agt Ser Cys Ser 305			921

<210> 27  
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 <212> PRT  
 <213> Felis catus

<400> 27

Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His

1	5	10	15
Pro Asp Ala	Pro Gly Glu Met Val	Val Leu Thr Cys Asn Thr	Pro Glu
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Glu Asp Asp	Ile Thr Trp Thr Ser Asp	Gln Ser Ser Glu Val Leu Gly	
	35	40	45
Ser Gly Lys	Thr Leu Thr Ile Gln Val Lys Glu	Phe Ala Asp Ala Gly	
	50	55	60
Gln Tyr Thr	Cys His Lys Gly Gly Glu Val Leu Ser	His Ser Phe Leu	
	65	70	75
Leu Ile His	Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp	Ile Leu Arg	
	85	90	95
Glu Gln Lys	Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys	Glu Ala Lys	
	100	105	110
Asn Tyr Ser	Gly Arg Phe Thr Cys Trp Trp Leu Thr	Ala Ile Ser Thr	
	115	120	125
Asp Leu Lys	Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp	Pro Gln	
	130	135	140
Glu Val Thr	Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg	Val	
	145	150	155
Asp Asn Arg	Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser		
	165	170	175
Ala Cys Pro	Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp		
	180	185	190
Ala Ile His	Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile		
	195	200	205
Arg Asp Ile	Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro		
	210	215	220
Leu Lys Asn	Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr		
	225	230	235
			240

IM-5  
 Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val  
                   245                  250                  255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys  
                   260                  265                  270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln  
                   275                  280                  285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val  
                   290                  295                  300

Ser Cys Ser  
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 tctgtctttc ttttctctgt tgttcttgcc ctggacctgt acgccaaatg ttaaggagaa 180  
 gtaggaatgt ggggtgctcc aggtgtcagg gtattcccag ctcaactcca catgccgaga 240  
 attttttaat ggcttcagtt gcaggttctt ggggtgggtcc ggtttgatga tgtccctgat 300  
 gaagaagctg ctggtgtagt tttcgtactt gagcttgtga atagcgtcca ccacgacttc 360  
 aatgggtagg ctctcctcgg cagccgggca ggcactgccc tcctgacact ccactgtgta 420  
 cttcttataa tccctgttgt ccactctgac cttctctgct gagagtgtcg ctgctccaca 480  
 agtcacctct tgggggtcag aggagcctct gctgcttttg acagtgaatt tcaaatacgg 540  
 actgattgcc gtcagccacc agcaggtgaa acgtccagaa taattctttg cctcacattt 600  
 tagaaagatc ttatttttgg attctttctg ttcctttaag atatcagtgg accaaattcc 660  
 atcttccttt ttgtgtatca ggaggaacga atggctcaga acctcgctc ctttatgaca 720  
 ggtatactgg ccagcatctg caaattcttt gacttggatg gtcagagttt taccagagcc 780  
 taggacttca ctgctctggt cagaggtcca ggtgatgtca tcttcttcag gagtattgca 840  
 ggtgaggacc accatttctc cgggggcatc aggggtgccag tccaactcta caacataaac 900  
 gtttttctcc agttcccata t 921

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 1 5 10 15  
 gca cct ccc ctg atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt 96  
 Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val  
 20 25 30  
 gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctg 144  
 Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
 35 40 45  
 acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag 192  
 Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln  
 50 55 60  
 agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa 240  
 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
 65 70 75 80  
 gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt 288  
 Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val  
 85 90 95  
 ctg agc cat tcg ttc ctg ctg ata cac aaa aag gaa gat gga att tgg 336  
 Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
 100 105 110  
 tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt 384  
 Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
 115 120 125  
 cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg 432  
 Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
 130 135 140  
 ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga 480  
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg  
 145 150 155 160  
 ggc tcc tct gac ccc caa ggg gtg act tgt gga gca gcg aca ctg tca 528  
 Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser  
 165 170 175  
 gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg 576  
 Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
 180 185 190

## IM-5

gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc 624  
 Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro  
 195 200 205  
  
 att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac 672  
 Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
 210 215 220  
  
 acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag 720  
 Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys  
 225 230 235 240  
  
 aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc 768  
 Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
 245 250 255  
  
 tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta 816  
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
 260 265 270  
  
 aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac 864  
 Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
 275 280 285  
  
 aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat 912  
 Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp  
 290 295 300  
  
 gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg 960  
 Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
 305 310 315 320  
  
 agc aac tgg gca tcc gtg tcc tgc agt 987  
 Ser Asn Trp Ala Ser Val Ser Cys Ser  
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<210> 30  
 <211> 329  
 <212> PRT  
 <213> Felis catus

<400> 30

Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu  
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Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val  
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
35 40 45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln  
50 55 60

## IM-5

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val  
85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg  
145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser  
165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro  
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys  
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp

290

295

300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
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Ser Asn Trp Ala Ser Val Ser Cys Ser  
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 tctgtctttc ttttctctgt tgttcttgcc ctggacctgt acgccaaatg ttaaggagaa 180  
 gtaggaatgt ggggtgctcc aggtgtcagg gtattcccag ctcaactcca catgccgaga 240  
 attttttaat ggcttcagtt gcaggttctt ggggtgggtcc ggtttgatga tgtccctgat 300  
 gaagaagctg ctggtgtagt tttcgtactt gagcttgtga atagcgtcca ccacgacttc 360  
 aatgggtagg ctctcctcgg cagccgggca ggcactgccc tcttgacact cactgtgta 420  
 cttcttataa tccctgttgt cactctgac cttctctgct gagagtgtcg ctgctccaca 480  
 agtcaccctt tgggggtcag aggagcctct gctgcttttg acagtgaatt tcaaactcgg 540  
 actgattgcc gtcagccacc agcaggtgaa acgtccagaa taattctttg cctcacattt 600  
 tagaaagatc ttatttttgg attctttctg ttcccttaag atatcagtgg accaaattcc 660  
 atcttccttt ttgtgtatca ggaggaacga atggctcaga acctcgctc ctttatgaca 720  
 ggtatactgg ccagcatctg caaattcttt gacttggatg gtcagagttt taccagagcc 780  
 taggacttca ctgctctggt cagaggtcca ggtgatgtca tcttcttcag gagtattgca 840  
 ggtgaggacc accatttctc cgggggcatc agggtgccag tccaactcta caacataaac 900  
 gtttttctcc agttcccata tggccatgag gggaggtgcc agcaaaacca gggaaaacca 960  
 ggcgatgacc aactgctgag gatgcat 987

<210> 32  
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 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS



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&lt;223&gt;

&lt;400&gt; 32

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Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu	
1 5 10 15	
aac cac ctg gac cac ctc agt ttg gcc agg aac ctc ccc aca ccc aca	96
Asn His Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Thr Pro Thr	
20 25 30	
cca agc cca gga atg ttc cag tgc ctc aac cac tcc caa acc ctg ctg	144
Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu	
35 40 45	
cga gcc atc agc aac acg ctt cag aag gcc aga caa act cta gaa ttt	192
Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe	
50 55 60	
tac tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aaa gat	240
Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp	
65 70 75 80	
aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat	288
Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn	
85 90 95	
gag agt tgc ctg gct tcc aga gag atc tct ctg ata act aat ggg agt	336
Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser	
100 105 110	
tgc ctg gcc tcc aga aag acc tct ttt atg acg acc ctg tgc ctt agc	384
Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser	
115 120 125	
agt atc tat gag gac ttg aag atg tac cag gtg gag ttc aag gcc atg	432
Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met	
130 135 140	
aat gca aag ctg tta atg gat cct aaa agg cag atc ttt ctg gat caa	480
Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln	
145 150 155 160	
aac atg ctg aca gct att gat gag ctg tta cag gcc ctg aat gtc aac	528
Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn	
165 170 175	
agt gtg act gtg cca cag aac tcc tcc ctg gaa gaa ccg gat ttt tat	576
Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr	
180 185 190	
aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt	624
Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg	
195 200 205	
gca gtg acc atc aat aga atg atg agc tat ctg aat gct tcc	666
Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser	

210

215

220

<210> 33  
 <211> 222  
 <212> PRT  
 <213> Felis catus

<400> 33

Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu  
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 20 25 30

Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu  
 35 40 45

Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe  
 50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp  
 65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn  
 85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser  
 100 105 110

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser  
 115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met  
 130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln  
 145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn  
 165 170 175

Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr  
 180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg

195

200

205

Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser  
 210 215 220

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 <211> 666  
 <212> DNA  
 <213> Felis catus

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 ctgtggcaca gtcacactgt tgacattcag ggctgtaac agtcatcaa tagctgtcag 180  
 catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240  
 cttgaactcc acctggtaca ttttcaagtc ctcatagata ctgctaaggc acagggctcg 300  
 cataaaagag gtctttcttg aggccaggca actcccatta gttatcagag agatctctct 360  
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 gggttttatct tttgtgatat cttcatgac aatctcttcg gaagtgcagg agtaaaattc 480  
 tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg 540  
 gttgaggcac tggaacattc ctgggcttgg tgtgggtgtg gggagggtcc tggccaaact 600  
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 gcacat 666

<210> 35  
 <211> 591  
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 1 5 10 15  
 aac cac tcc caa acc ctg ctg cga gcc atc agc aac acg ctt cag aag 96  
 Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys  
 20 25 30  
 gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat 144

IM-5

Ala	Arg	Gln	Thr	Leu	Glu	Phe	Tyr	Ser	Cys	Thr	Ser	Glu	Glu	Ile	Asp	
		35					40					45				
cat	gaa	gat	atc	aca	aaa	gat	aaa	acc	agc	aca	gtg	gag	gcc	tgc	tta	192
His	Glu	Asp	Ile	Thr	Lys	Asp	Lys	Thr	Ser	Thr	Val	Glu	Ala	Cys	Leu	
	50					55					60					
cca	ctg	gaa	tta	acc	atg	aat	gag	agt	tgc	ctg	gct	tcc	aga	gag	atc	240
Pro	Leu	Glu	Leu	Thr	Met	Asn	Glu	Ser	Cys	Leu	Ala	Ser	Arg	Glu	Ile	
65					70				75						80	
tct	ctg	ata	act	aat	ggg	agt	tgc	ctg	gcc	tcc	aga	aag	acc	tct	ttt	288
Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala	Ser	Arg	Lys	Thr	Ser	Phe	
				85				90						95		
atg	acg	acc	ctg	tgc	ctt	agc	agt	atc	tat	gag	gac	ttg	aag	atg	tac	336
Met	Thr	Thr	Leu	Cys	Leu	Ser	Ser	Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr	
			100					105					110			
cag	gtg	gag	ttc	aag	gcc	atg	aat	gca	aag	ctg	tta	atg	gat	cct	aaa	384
Gln	Val	Glu	Phe	Lys	Ala	Met	Asn	Ala	Lys	Leu	Leu	Met	Asp	Pro	Lys	
		115					120					125				
agg	cag	atc	ttt	ctg	gat	caa	aac	atg	ctg	aca	gct	att	gat	gag	ctg	432
Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu	Thr	Ala	Ile	Asp	Glu	Leu	
	130					135					140					
tta	cag	gcc	ctg	aat	gtc	aac	agt	gtg	act	gtg	cca	cag	aac	tcc	tcc	480
Leu	Gln	Ala	Leu	Asn	Val	Asn	Ser	Val	Thr	Val	Pro	Gln	Asn	Ser	Ser	
145				150						155					160	
ttg	gaa	gaa	ccg	gat	ttt	tat	aaa	act	aaa	atc	aag	ctc	tgc	ata	ctt	528
Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu	
				165					170					175		
ctt	cat	gct	ttc	aga	att	cgt	gca	gtg	acc	atc	aat	aga	atg	atg	agc	576
Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr	Ile	Asn	Arg	Met	Met	Ser	
			180					185					190			
tat	ctg	aat	gct	tcc												591
Tyr	Leu	Asn	Ala	Ser												
		195														

<210> 36  
 <211> 197  
 <212> PRT  
 <213> Felis catus

<400> 36

Arg	Asn	Leu	Pro	Thr	Pro	Thr	Pro	Ser	Pro	Gly	Met	Phe	Gln	Cys	Leu
1				5					10					15	

Asn	His	Ser	Gln	Thr	Leu	Leu	Arg	Ala	Ile	Ser	Asn	Thr	Leu	Gln	Lys
			20					25					30		

## IM-5

Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp  
35 40 45

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu  
50 55 60

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile  
65 70 75 80

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe  
85 90 95

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr  
100 105 110

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys  
115 120 125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu  
130 135 140

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser  
145 150 155 160

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu  
165 170 175

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser  
180 185 190

Tyr Leu Asn Ala Ser  
195

<210> 37

<211> 591

<212> DNA

<213> Felis catus

<400> 37

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aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca aggaggagtt 120

ctgtggcaca gtcacactgt tgacattcag ggctgtaac agctcatcaa tagctgtcag 180

catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240

cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300

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cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctctct 360
ggaagccagg caactctcat tcatgggttaa ttccagtggg aagcaggcct ccactgtgct 420
ggttttctct tttgtgatat ctccatgata aatctcttcg gaagtgcagg agtaaaattc 480
tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg 540
gttgaggcac tggaacattc ctgggcttgg tgtgggtgtg gggaggttcc t 591

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<210> 38
<211> 1599
<212> DNA
<213> Felis catus

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<220>
<221> CDS
<222> (1)..(1599)
<223>

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Met His Pro Gln Gln Leu Val Ile Ala Trp Leu Ser Leu Val Leu Leu
1 5 10 15

gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt 96
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
20 25 30

gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc 144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag 192
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
50 55 60

agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa 240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65 70 75 80

gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt 288
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
85 90 95

ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg 336
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
100 105 110

tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt 384
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
115 120 125

cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg 432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
130 135 140

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## IM-5

ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg 145 150 155 160	480
ggc tcc tct gac ccc caa gag gtg act tgt gga gca gcg aca ctc tca Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser 165 170 175	528
gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val 180 185 190	576
gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro 195 200 205	624
att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr 210 215 220	672
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys 225 230 235 240	720
aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser 245 250 255	768
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu 260 265 270	816
aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp 275 280 285	864
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp 290 295 300	912
gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp 305 310 315 320	960
agc aac tgg gca tcc gtg tcc tgc agt ggt ggc ggt ggc ggc gga tct Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser 325 330 335	1008
aga aac ttg cca acc cct act cca tcc ccg ggg atg ttc cag tgc ctc Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu 340 345 350	1056
aac cac tcc caa acc ctg ctg cga gcc atc agc aac acg ctt cag aag Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys 355 360 365	1104
gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp	1152

## IM-5

370	375	380	
cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag gcc tgc tta			1200
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu			
385	390	395	400
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc			1248
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile			
405	410	415	
tct ctg ata act aat ggg agt tgc ctg gcc tcc aga aag acc tct ttt			1296
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe			
420	425	430	
atg acg acc ctg tgc ctt agc agt atc tat gag gac ttg aag atg tac			1344
Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr			
435	440	445	
cag gtg gag ttc aag gcc atg aat gca aag ctg tta atg gat cct aaa			1392
Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys			
450	455	460	
agg cag atc ttt ctg gat caa aac atg ctg aca gct att gat gag ctg			1440
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu			
465	470	475	480
tta cag gcc ctg aat gtc aac agt gtg act gtg cca cag aac tcc tcc			1488
Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser			
485	490	495	
ttg gaa gaa ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt			1536
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu			
500	505	510	
ctt cat gct ttc aga att cgt gca gtg acc atc aat aga atg atg agc			1584
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser			
515	520	525	
tat ctg aat gct tcc			1599
Tyr Leu Asn Ala Ser			
530			

<210> 39  
 <211> 533  
 <212> PRT  
 <213> Felis catus

<400> 39

Met	His	Pro	Gln	Gln	Leu	Val	Ile	Ala	Trp	Leu	Ser	Leu	Val	Leu	Leu
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Ala	Pro	Pro	Leu	Met	Ala	Ile	Trp	Glu	Leu	Glu	Lys	Asn	Val	Tyr	Val
			20					25					30		

Val	Glu	Leu	Asp	Trp	His	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



35

40

45

Thr	Cys	Asn	Thr	Pro	Glu	Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Asp	Gln
50						55					60				
Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
65					70					75					80
Glu	Phe	Ala	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val
				85					90					95	
Leu	Ser	His	Ser	Phe	Leu	Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp
			100					105					110		
Ser	Thr	Asp	Ile	Leu	Arg	Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe
		115					120					125			
Leu	Lys	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp
	130					135					140				
Leu	Thr	Ala	Ile	Ser	Thr	Asp	Leu	Lys	Phe	Thr	Val	Lys	Ser	Ser	Arg
145					150					155					160
Gly	Ser	Ser	Asp	Pro	Gln	Glu	Val	Thr	Cys	Gly	Ala	Ala	Thr	Leu	Ser
				165					170					175	
Ala	Glu	Lys	Val	Arg	Val	Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val
			180					185					190		
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro
	195						200				205				
Ile	Glu	Val	Val	Val	Asp	Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr
	210					215					220				
Thr	Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys
225					230					235					240
Asn	Leu	Gln	Leu	Lys	Pro	Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser
				245					250					255	
Trp	Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu
			260					265					270		

## IM-5

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
 275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp  
 290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
 305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser  
 325 330 335

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu  
 340 345 350

Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys  
 355 360 365

Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp  
 370 375 380

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu  
 385 390 395 400

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile  
 405 410 415

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe  
 420 425 430

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr  
 435 440 445

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys  
 450 455 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu  
 465 470 475 480

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser  
 485 490 495

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu  
 500 505 510

## IM-5

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser  
 515 520 525

Tyr Leu Asn Ala Ser  
 530

<210> 40  
 <211> 1599  
 <212> DNA  
 <213> Felis catus

<400> 40  
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 aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca aggaggagt 120  
 ctgtggcaca gtcacactgt tgacattcag ggctgtaac agctcatcaa tagctgtcag 180  
 catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240  
 cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggctcg 300  
 cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctctct 360  
 ggaagccagg caactctcat tcatgggttaa ttccagtggc aagcaggcct ccactgtgct 420  
 ggttttatct tttgtgatat ctcatgatc aatctcttcg gaagtgcagg agtaaaattc 480  
 tagagtttgt ctggccttct gaagcgtggt gctgatggc cgcagcaggg tttgggagt 540  
 gttgaggcac tggaacatcc ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600  
 gccaccgcca ccactgcagg acacggatgc ccagttgctc caggatgagc tatagtagcg 660  
 gtctctggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720  
 gtccacggag agtctgtctt tcttttctct gttgttcttg ccctggacct gtacgccaaa 780  
 tgttaaggag aagtaggaat gtgggggtgct ccaggtgtca gggattccc agctcacttc 840  
 cacatgccga gaatttttta atggcttcag ttgcagggtc ttgggtgggt ccggtttgat 900  
 gatgtccctg atgaagaagc tgctgggtga gttttcgtac ttgagcttgt gaatagcgtc 960  
 caccacgact tcaatgggta ggctctctc gccagccggg caggcactgc cctctgaca 1020  
 ctccactgtg tacttcttat aatccctgtt gtccactctg accttctctg ctgagagtgt 1080  
 cgctgtcca caagtcacct cttgggggtc agaggagcct ctgctgcttt tgacagtga 1140  
 tttcaaactg gtactgattg ccgtcagcca ccagcaggtg aaacgtccag aataattctt 1200  
 tgctcacat tttagaaaga tcttattttt ggattcttct tgttccctta agatatcagt 1260  
 ggaccaaatt ccattcttct ttttgtgtat caggaggaac gaatggctca gaacctcgcc 1320

## IM-5

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 ttaccagag cctaggactt cactgctctg gtcagaggtc caggtgatgt catcttcttc 1440  
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 <212> DNA  
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 aagactcaaa ttgtatctta tcatcatgtc ctggaacact tctctgaaag aatatgatgt 180  
 catttcttc atcattgata ctctcaggag gactcatttc cttaaaggaa ataattttgt 240  
 tctcacagga gagagtagac atgggtcttat aattcacaga gatgggttact gccagacctc 300  
 tagtgaggct atctttatac atatatatga taaattcagt ccgggggtgca ttatctgtac 360  
 agtcagaatc aggcataatc tcaaacacag gttgatctcc ctgggttaatg aagagaactt 420  
 ggtcgttcaa gtttcgtaag attgagagtt tatgttcaag cttgccaaag taatctgttt 480  
 ccagggtttc atcactgtca gctacaaagt aaagtgtatt gtcaataaat ttcattccca 540  
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<210> 42  
 <211> 0  
 <212> DNA  
 <213> Felis catus

<400> 42  
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<210> 43  
 <211> 1533  
 <212> DNA  
 <213> Felis catus

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 <221> CDS  
 <222> (1)..(1533)  
 <223>

<400> 43  
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IM-5																
Ile	Trp	Glu	Leu	Glu	Lys	Asn	Val	Tyr	Val	Val	Glu	Leu	Asp	Trp	His	
1				5					10					15		
cct	gat	gcc	ccc	gga	gaa	atg	gtg	gtc	ctc	acc	tgc	aat	act	cct	gaa	96
Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu	Thr	Cys	Asn	Thr	Pro	Glu	
			20					25					30			
gaa	gat	gac	atc	acc	tgg	acc	tct	gac	cag	agc	agt	gaa	gtc	cta	ggc	144
Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Asp	Gln	Ser	Ser	Glu	Val	Leu	Gly	
		35					40					45				
tct	ggg	aaa	act	ctg	acc	atc	caa	gtc	aaa	gaa	ttt	gca	gat	gct	ggc	192
Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys	Glu	Phe	Ala	Asp	Ala	Gly	
	50					55					60					
cag	tat	acc	tgt	cat	aaa	gga	ggc	gag	gtt	ctg	agc	cat	tcg	ttc	ctc	240
Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val	Leu	Ser	His	Ser	Phe	Leu	
65					70					75					80	
ctg	ata	cac	aaa	aag	gaa	gat	gga	att	tgg	tcc	act	gat	atc	tta	agg	288
Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	Ser	Thr	Asp	Ile	Leu	Arg	
				85					90					95		
gaa	cag	aaa	gaa	tcc	aaa	aat	aag	atc	ttt	cta	aaa	tgt	gag	gca	aag	336
Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	Leu	Lys	Cys	Glu	Ala	Lys	
			100					105					110			
aat	tat	tct	gga	cgt	ttc	acc	tgc	tgg	tgg	ctg	acg	gca	atc	agt	acc	384
Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu	Thr	Ala	Ile	Ser	Thr	
		115					120					125				
gat	ttg	aaa	ttc	act	gtc	aaa	agc	agc	aga	ggc	tcc	tct	gac	ccc	caa	432
Asp	Leu	Lys	Phe	Thr	Val	Lys	Ser	Ser	Arg	Gly	Ser	Ser	Asp	Pro	Gln	
	130					135					140					
gag	gtg	act	tgt	gga	gca	gcg	aca	ctc	tca	gca	gag	aag	gtc	aga	gtg	480
Glu	Val	Thr	Cys	Gly	Ala	Ala	Thr	Leu	Ser	Ala	Glu	Lys	Val	Arg	Val	
145					150					155					160	
gac	aac	agg	gat	tat	aag	aag	tac	aca	gtg	gag	tgt	cag	gag	ggc	agt	528
Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	Glu	Cys	Gln	Glu	Gly	Ser	
				165					170					175		
gcc	tgc	ccg	gct	gcc	gag	gag	agc	cta	ccc	att	gaa	gtc	gtg	gtg	gac	576
Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Asp	
			180					185					190			
gct	att	cac	aag	ctc	aag	tac	gaa	aac	tac	acc	agc	agc	ttc	ttc	atc	624
Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile	
		195					200						205			
agg	gac	atc	atc	aaa	ccg	gac	cca	ccc	aag	aac	ctg	caa	ctg	aag	cca	672
Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn	Leu	Gln	Leu	Lys	Pro	
	210					215					220					
tta	aaa	aat	tct	cgg	cat	gtg	gaa	gtg	agc	tgg	gaa	tac	cct	gac	acc	720
Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr	
225					230					235					240	

tgg	agc	acc	cca	cat	tcc	tac	ttc	tcc	tta	aca	ttt	ggc	gta	cag	gtc	768
Trp	Ser	Thr	Pro	His 245	Ser	Tyr	Phe	Ser	Leu 250	Thr	Phe	Gly	Val	Gln 255	Val	
cag	ggc	aag	aac	aac	aga	gaa	aag	aaa	gac	aga	ctc	tcc	gtg	gac	aag	816
Gln	Gly	Lys	Asn 260	Asn	Arg	Glu	Lys	Lys 265	Asp	Arg	Leu	Ser	Val 270	Asp	Lys	
acc	tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	864
Thr	Ser	Ala 275	Lys	Val	Val	Cys	His 280	Lys	Asp	Ala	Lys	Ile 285	Arg	Val	Gln	
gcc	aga	gac	cgc	tac	tat	agc	tca	tcc	tgg	agc	aac	tgg	gca	tcc	gtg	912
Ala	Arg 290	Asp	Arg	Tyr	Tyr	Ser 295	Ser	Ser	Trp	Ser	Asn 300	Trp	Ala	Ser	Val	
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Ser 305	Cys	Ser	Gly 310	Gly	Gly	Gly	Gly	Ser	Arg 315	Asn	Leu	Pro	Thr	Pro 320		
act	cca	tcc	ccg	ggg	atg	ttc	cag	tgc	ctc	aac	cac	tcc	caa	acc	ctg	1008
Thr	Pro	Ser	Pro	Gly 325	Met	Phe	Gln	Cys	Leu 330	Asn	His	Ser	Gln	Thr 335	Leu	
ctg	cga	gcc	atc	agc	aac	acg	ctt	cag	aag	gcc	aga	caa	act	cta	gaa	1056
Leu	Arg	Ala	Ile 340	Ser	Asn	Thr	Leu	Gln 345	Lys	Ala	Arg	Gln	Thr 350	Leu	Glu	
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Phe	Tyr	Ser 355	Cys	Thr	Ser	Glu	Glu	Ile 360	Asp	His	Glu	Asp 365	Ile	Thr	Lys	
gat	aaa	acc	agc	aca	gtg	gag	gcc	tgc	tta	cca	ctg	gaa	tta	acc	atg	1152
Asp	Lys 370	Thr	Ser	Thr	Val	Glu 375	Ala	Cys	Leu	Pro	Leu 380	Glu	Leu	Thr	Met	
aat	gag	agt	tgc	ctg	gct	tcc	aga	gag	atc	tct	ctg	ata	act	aat	ggg	1200
Asn 385	Glu	Ser	Cys	Leu	Ala 390	Ser	Arg	Glu	Ile	Ser 395	Leu	Ile	Thr	Asn	Gly 400	
agt	tgc	ctg	gcc	tcc	aga	aag	acc	tct	ttt	atg	acg	acc	ctg	tgc	ctt	1248
Ser	Cys	Leu	Ala 405	Ser	Arg	Lys	Thr	Ser	Phe 410	Met	Thr	Thr	Leu	Cys 415	Leu	
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Ser	Ser	Ile	Tyr 420	Glu	Asp	Leu	Lys	Met 425	Tyr	Gln	Val	Glu	Phe 430	Lys	Ala	
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Met	Asn 435	Ala	Lys	Leu	Leu	Met	Asp 440	Pro	Lys	Arg	Gln	Ile 445	Phe	Leu	Asp	
caa	aac	atg	ctg	aca	gct	att	gat	gag	ctg	tta	cag	gcc	ctg	aat	gtc	1392
Gln 450	Asn	Met	Leu	Thr	Ala 455	Ile	Asp	Glu	Leu	Leu	Gln 460	Ala	Leu	Asn	Val	
aac	agt	gtg	act	gtg	cca	cag	aac	tcc	tcc	ttg	gaa	gaa	ccg	gat	ttt	1440
Asn 465	Ser	Val	Thr	Val 470	Pro	Gln	Asn	Ser	Ser	Leu 475	Glu	Glu	Pro	Asp 480	Phe	

## IM-5

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 Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile  
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cgt gca gtg acc atc aat aga atg atg agc tat ctg aat gct tcc 1533  
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Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu  
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Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly  
                     35                    40                    45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly  
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Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu  
 65                    70                    75                    80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg  
                     85                    90                    95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys  
                     100                    105                    110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr  
                     115                    120                    125

Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln  
                     130                    135                    140

Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val  
 145                    150                    155                    160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser  
                     165                    170                    175

## IM-5

Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp  
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Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile  
 195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro  
 210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr  
 225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val  
 245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys  
 260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln  
 275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val  
 290 295 300

Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro  
 305 310 315 320

Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu  
 325 330 335

Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu  
 340 345 350

Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys  
 355 360 365

Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met  
 370 375 380

Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly  
 385 390 395 400

Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu



									IM-5							
				405					410						415	
Ser	Ser	Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr	Gln	Val	Glu	Phe	Lys	Ala	
			420					425					430			
Met	Asn	Ala	Lys	Leu	Leu	Met	Asp	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	
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Gln	Asn	Met	Leu	Thr	Ala	Ile	Asp	Glu	Leu	Leu	Gln	Ala	Leu	Asn	Val	
	450					455					460					
Asn	Ser	Val	Thr	Val	Pro	Gln	Asn	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	
465					470					475					480	
Tyr	Lys	Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	
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gccaccgcca	ccactgcagg	acacggatgc	ccagttgctc	caggatgagc	tatagtagcg	660	
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gatgtccctg atgaagaagc tgctgggtgta gttttcgtac ttgagcttgt gaatagcgtc	960
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ggaccaaatt ccatcttcct ttttgtgtat caggaggaac gaatggctca gaacctcgcc	1320
tcctttatga caggtatact ggccagcatc tgcaaattct ttgacttggg tggtcagagt	1380
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1 5 10 15	
agc cac ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca	96
Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser	
20 25 30	
ccg agc cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg	144
Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu	
35 40 45	
aga gcc gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta	192
Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu	
50 55 60	
tat tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aag gat	240
Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp	
65 70 75 80	



## IM-5

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp  
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn  
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser  
100 105 110

Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser  
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met  
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln  
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn  
165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr  
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Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg  
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cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300  
cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360

## IM-5

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 tagagtttgt ctggccttct gaagcgtggt gctgacggct ctcagcaggt tttgggagtg 540  
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 aac cac tcc caa aac ctg ctg aga gcc gtc agc aac acg ctt cag aag 96  
 Asn His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys  
 20 25 30  
 gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat 144  
 Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp  
 35 40 45  
 cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta 192  
 His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu  
 50 55 60  
 cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc 240  
 Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile  
 65 70 75 80  
 tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt 288  
 Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe  
 85 90 95  
 atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac 336  
 Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr  
 100 105 110  
 cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag 384  
 Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys  
 115 120 125  
 agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg 432  
 Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu

## IM-5

130	135	140	
tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc			480
Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser			
145	150	155	160
ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt			528
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu			
	165	170	175
ctt cat gct ttc aga att cgt gcg gtg acc atc gat aga atg atg agt			576
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Met Met Ser			
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tat ctg aat tct tcc			591
Tyr Leu Asn Ser Ser			
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Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp
35 40 45

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
50 55 60

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
65 70 75 80

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe
85 90 95

Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr
100 105 110

Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys
115 120 125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu
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130

135

140

Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser  
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Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu  
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Tyr Leu Asn Ser Ser  
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 ctgtggcaca gtcacactgt tgaaattcag ggccctgtaac agctcatcga tagctgtcag 180  
 catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240  
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 tagagtttgt ctggccttct gaagcgtggt gctgacggct ctcagcaggt tttgggagtg 540  
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IM-5

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cag ggc aag aac aat aga gaa aag aaa gat aga ctc tgc gtg gac aag	816
Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys	
260 265 270	
acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa	864
Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln	
275 280 285	
gcc cga gac cgc tac tat agt tca tcc tgg agc gac tgg gca tct gtg	912
Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val	
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tcc tgc agt	921
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35 40 45	
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly	
50 55 60	
Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu	
65 70 75 80	
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys	
85 90 95	
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys	
100 105 110	
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr	
115 120 125	

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Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln  
 130 135 140

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val  
 145 150 155 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser  
 165 170 175

Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp  
 180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile  
 195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro  
 210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr  
 225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala  
 245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys  
 260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln  
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Ser Cys Ser  
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## IM-5

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 Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu  
 1 5 10 15  
 gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt 96  
 Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val  
 20 25 30  
 gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc 144  
 Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
 35 40 45  
 acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag 192  
 Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln  
 50 55 60  
 agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa 240  
 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys



## IM-5

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
 305 310 315 320

agc aac tgg gca tcc gtg tcc tgc a  
 Ser Asn Trp Ala Ser Val Ser Cys  
 325

985

<210> 56  
 <211> 328  
 <212> PRT  
 <213> Felis catus

<400> 56

Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu  
 1 5 10 15

Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val  
 20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
 35 40 45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln  
 50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
 65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val  
 85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
 100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
 115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
 130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg  
 145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser  
 165 170 175

## IM-5

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
 180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro  
 195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
 210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys  
 225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
 245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
 260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
 275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp  
 290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
 305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys  
 325

<210> 57  
 <211> 985  
 <212> DNA  
 <213> Felis catus

<400> 57  
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 cgcggatctt ggcatacctt tggcacacga ccttggtctga ggtcttgtcc acggagagtc 120  
 tgtctttctt ttctctgttg ttcttgccct ggacctgtac gccaaatgtt aaggagaagt 180  
 aggaatgtgg ggtgctccag gtgtcagggt attcccagct cacttcaca tgccgagaat 240  
 tttttaatgg cttcagttgc aggttcttgg gtgggtccgg tttgatgatg tcctgatga 300  
 agaagctgct ggtgtagttt tcgtacttga gcttgtgaat agcgtccacc acgacttcaa 360  
 tgggtaggct ctctcggca gccgggcagg cactgcctc ctgacactcc actgtgtact 420

tcttataatc cctgttggtcc actctgacct tctctgctga gagtgtcgct gctccacaag 480  
 tcaccccttg ggggtcagag gagcctctgc tgcttttgac agtgaatttc aaatcggtac 540  
 tgattgccgt cagccaccag caggtgaaac gtccagaata attctttgcc tcacatttta 600  
 gaaagatctt atttttggat tctttctggt cccttaagat atcagtggac caaatcccat 660  
 ctctcttttt gtgtatcagg aggaacgaat ggctcagaac ctgcctcct ttatgacagg 720  
 tatactggcc agcatctgca aattctttga cttggatggc cagagtttta ccagagccta 780  
 ggacttcaact gctctgggtca gaggtccagg tgatgtcacc ttcttcagga gtattgcagg 840  
 tgaggaccac catttctccg ggggcatcag ggtgccagtc caactctaca acataaacgt 900  
 ttttctccag tccccatatg gccatgaggg gaggtgccag caaaaccagg gaaaaccagg 960  
 cgatgaccaa ctgctgagga tgcac 985

<210> 58  
 <211> 987  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(987)  
 <223>

<400> 58  
 atg cac cct cag cag ttg gtc atc tcc tgg ttt tcc ctc gtt ttg ctg 48  
 Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu  
 1 5 10 15  
 gcg tct ccc ctc atg gcc ata tgg gaa ctg gag aaa gat gtt tat gtt 96  
 Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val  
 20 25 30  
 gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc 144  
 Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
 35 40 45  
 acc tgc cat acc cct gaa gaa gat gac atc act tgg acc tca gcg cag 192  
 Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln  
 50 55 60  
 agc agt gaa gtc cta ggt tct ggt aaa act ctg acc atc caa gtc aaa 240  
 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
 65 70 75 80  
 gaa ttt gga gat gct ggc cag tat acc tgc cat aaa gga ggc aag gtt 288  
 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val  
 85 90 95  
 ctg agc cgc tca ctc ctg ttg att cac aaa aaa gaa gat gga att tgg 336

IM-5																
Leu	Ser	Arg	Ser	Leu	Leu	Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	
			100					105					110			
tcc	act	gat	atc	tta	aag	gaa	cag	aaa	gaa	tcc	aaa	aat	aag	atc	ttt	384
Ser	Thr	Asp	Ile	Leu	Lys	Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	
		115					120					125				
ctg	aaa	tgt	gag	gca	aag	aat	tat	tct	gga	cgt	ttc	aca	tgc	tgg	tgg	432
Leu	Lys	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	
	130					135					140					
ctg	acg	gca	atc	agt	act	gat	ttg	aaa	ttc	agt	gtc	aaa	agt	agc	aga	480
Leu	Thr	Ala	Ile	Ser	Thr	Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg	
145					150					155					160	
ggc	ttc	tct	gac	ccc	caa	ggg	gtg	aca	tgt	gga	gca	gtg	aca	ctt	tca	528
Gly	Phe	Ser	Asp	Pro	Gln	Gly	Val	Thr	Cys	Gly	Ala	Val	Thr	Leu	Ser	
			165						170					175		
gca	gag	agg	gtc	aga	gtg	gac	aac	agg	gat	tat	aag	aag	tac	aca	gtg	576
Ala	Glu	Arg	Val	Arg	Val	Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	
			180					185					190			
gag	tgt	cag	gag	ggc	agt	gcc	tgc	ccc	tct	gcc	gag	gag	agc	cta	ccc	624
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	
		195				200						205				
atc	gag	gtc	gtg	gtg	gat	gct	att	cac	aag	ctc	aag	tat	gaa	aac	tac	672
Ile	Glu	Val	Val	Val	Asp	Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	
	210					215					220					
acc	agc	agc	ttc	ttc	atc	aga	gac	atc	atc	aaa	cca	gac	cca	ccc	aca	720
Thr	Ser	Ser	Phe	Phe	Ile	Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	
225					230					235					240	
aac	ctg	cag	ctg	aag	cca	ttg	aaa	aat	tct	cgg	cac	gtg	gag	gtc	agc	768
Asn	Leu	Gln	Leu	Lys	Pro	Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	
				245				250					255			
tgg	gaa	tac	ccc	gac	acc	tgg	agc	acc	cca	cat	tcc	tac	ttc	tcc	ctg	816
Trp	Glu	Tyr	Pro	Asp	Thr	Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	
			260					265					270			
aca	ttt	tgc	ata	cag	gcc	cag	ggc	aag	aac	aat	aga	gaa	aag	aaa	gat	864
Thr	Phe	Cys	Ile	Gln	Ala	Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	
		275					280					285				
aga	ctc	tgc	gtg	gac	aag	acc	tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	912
Arg	Leu	Cys	Val	Asp	Lys	Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	
	290					295					300					
gcc	aag	atc	cgc	gtg	caa	gcc	cga	gac	cgc	tac	tat	agt	tca	tcc	tgg	960
Ala	Lys	Ile	Arg	Val	Gln	Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	
305					310					315					320	
agc	gac	tgg	gca	tct	gtg	tca	tgc	agt								987
Ser	Asp	Trp	Ala	Ser	Val	Ser	Cys	Ser								
				325												



## IM-5

<210> 59  
 <211> 329  
 <212> PRT  
 <213> Canis familiaris

<400> 59

Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu  
 1 5 10 15

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val  
 20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
 35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln  
 50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
 65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val  
 85 90 95

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
 100 105 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
 115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
 130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg  
 145 150 155 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser  
 165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
 180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro  
 195 200 205

IM-5

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr  
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
260 265 270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp  
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
305 310 315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser  
325

<210> 60  
<211> 987  
<212> DNA  
<213> Canis familiaris

<400> 60  
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cacgcggtac ttggcattct tgtggcacac gaccttggct gaggtcttgt ccacgcagag 120  
tctatctttc ttttctctat tgttcttgcc ctgggcctgt atgcaaaatg tcaggagaga 180  
gtaggaatgt ggggtgctcc aggtgtcggg gtattcccag ctgacctcca cgtgccgaga 240  
atTTTTcaat ggcttcagct gcagggttgt ggggtgggtct ggtttgatga tgtctctgat 300  
gaagaagctg ctggtgtagt tttcatactt gagcttgtga atagcatcca ccacgacctc 360  
gatgggtagg ctctcctcgg cagaggggca ggcactgccc tcctgacact cactgtgta 420  
cttcttataa tcctgttgt cactctgac cctctctgct gaaagtgtca ctgctccaca 480  
tgtcaccctt tgggggtcag agaagcctct gctacttttg acactgaatt tcaaatcagt 540  
actgattgcc gtcagccacc agcatgtgaa acgtccagaa taattctttg cctcacattt 600

## IM-5

cagaaagatc ttatTTTTtg attcttTctg ttccttTtaag atatcagtgg accaaattcc 660  
 atcttctttt ttgtgaatca acaggagtga gcggtctaga accttgcttc ctttatggca 720  
 ggtatactgg ccagcatctc caaattcttt gacttggatg gtcagagttt taccagaacc 780  
 taggacttca ctgctctgcg ctgagggtcca agtgatgtca tcttcttcag gggtatggca 840  
 ggtgaggacc accatttctc cgggggcctc aggggtgccag tccaactcta caacataaac 900  
 atcttctctc agttcccata tggccatgag gggagacgcc agcaaaacga gggaaaacca 960  
 ggagatgacc aactgctgag ggtgcat 987

<210> 61  
 <211> 1599  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(1599)  
 <223>

<400> 61  
 atg cac cct cag cag ttg gtc atc tcc tgg ttt tcc ctg gtt ttg ctg 48  
 Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu  
 1 5 10 15  
 gcg tct ccc ctg atg gcc ata tgg gaa ctg gag aaa gat gtt tat gtt 96  
 Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val  
 20 25 30  
 gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctg 144  
 Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
 35 40 45  
 acc tgc cat acc cct gaa gaa gat gac atc act tgg acc tca gcg cag 192  
 Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln  
 50 55 60  
 agc agt gaa gtc cta ggt tct ggt aaa act ctg acc atc caa gtc aaa 240  
 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
 65 70 75 80  
 gaa ttt gga gat gct ggc cag tat acc tgc cat aaa gga ggc aag gtt 288  
 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val  
 85 90 95  
 ctg agc cgc tca ctg ctg ttg att cac aaa aaa gaa gat gga att tgg 336  
 Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
 100 105 110  
 tcc act gat atc tta aag gaa cag aaa gaa tcc aaa aat aag atc ttt 384  
 Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
 115 120 125

ctg Leu	aaa Lys	tgt Cys	gag Glu	gca Ala	aag Lys	aat Asn	tat Tyr	tct Ser	gga Gly	cgt Arg	ttc Phe	aca Thr	tgc Cys	tgg Trp	tgg Trp	432
130135140																
ctg Leu	acg Thr	gca Ala	atc Ile	agt Ser	act Thr	gat Asp	ttg Leu	aaa Lys	ttc Phe	agt Ser	gtc Val	aaa Lys	agt Ser	agc Ser	aga Arg	480
145150155																
ggc Gly	ttc Phe	tct Ser	gac Asp	ccc Pro	caa Gln	ggg Gly	gtg Val	aca Thr	tgt Cys	gga Gly	gca Ala	gtg Val	aca Thr	ctt Leu	tca Ser	528
165170175																
gca Ala	gag Glu	agg Arg	gtc Val	aga Arg	gtg Val	gac Asp	aac Asn	agg Arg	gat Asp	tat Tyr	aag Lys	aag Lys	tac Tyr	aca Thr	gtg Val	576
180185190																
gag Glu	tgt Cys	cag Gln	gag Glu	ggc Gly	agt Ser	gcc Ala	tgc Cys	ccc Pro	tct Ser	gcc Ala	gag Glu	gag Glu	agc Ser	cta Leu	ccc Pro	624
195200205																
atc Ile	gag Glu	gtc Val	gtg Val	gtg Val	gat Asp	gct Ala	att Ile	cac His	aag Lys	ctc Leu	aag Lys	tat Tyr	gaa Glu	aac Asn	tac Tyr	672
210215220																
acc Thr	agc Ser	agc Ser	ttc Phe	ttc Phe	atc Ile	aga Arg	gac Asp	atc Ile	atc Ile	aaa Lys	cca Pro	gac Asp	cca Pro	ccc Pro	aca Thr	720
225230235																
aac Asn	ctg Leu	cag Gln	ctg Leu	aag Lys	cca Pro	ttg Leu	aaa Lys	aat Asn	tct Ser	cgg Arg	cac His	gtg Val	gag Glu	gtc Val	agc Ser	768
245250255																
tgg Trp	gaa Glu	tac Tyr	ccc Pro	gac Asp	acc Thr	tgg Trp	agc Ser	acc Thr	cca Pro	cat His	tcc Ser	tac Tyr	ttc Phe	tcc Ser	ctg Leu	816
260265270																
aca Thr	ttt Phe	tgc Cys	ata Ile	cag Gln	gcc Ala	cag Gln	ggc Gly	aag Lys	aac Asn	aat Asn	aga Arg	gaa Glu	aag Lys	aaa Lys	gat Asp	864
275280285																
aga Arg	ctc Leu	tgc Cys	gtg Val	gac Asp	aag Lys	acc Thr	tca Ser	gcc Ala	aag Lys	gtc Val	gtg Val	tgc Cys	cac His	aag Lys	gat Asp	912
290300																
gcc Ala	aag Lys	atc Ile	cgc Arg	gtg Val	caa Gln	gcc Ala	cga Arg	gac Asp	cgc Arg	tac Tyr	tat Tyr	agt Ser	tca Ser	tcc Ser	tgg Trp	960
305310315																
agc Ser	gac Asp	tgg Trp	gca Ala	tct Ser	gtg Val	tca Ser	tgc Cys	agt Ser	ggg Gly	ggc Gly	ggg Gly	ggc Gly	ggc Gly	gga Gly	tct Ser	1008
325330335																
aga Arg	aac Asn	ttg Leu	cca Pro	acc Thr	cct Pro	act Thr	cca Pro	tcc Ser	ccg Pro	ggg Gly	atg Met	ttc Phe	caa Gln	tgt Cys	ttg Leu	1056
340345350																
aac Asn	cac His	tcc Ser	caa Gln	acc Thr	ttg Leu	ttg Leu	aga Arg	gcc Ala	gtc Val	agc Ser	aac Asn	acg Thr	ctt Leu	cag Gln	aag Lys	1104
355360365																

## IM-5

gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat 1152  
 Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp  
 370 375 380

cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta 1200  
 His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu  
 385 390 395 400

cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc 1248  
 Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile  
 405 410 415

tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt 1296  
 Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe  
 420 425 430

atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac 1344  
 Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr  
 435 440 445

cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag 1392  
 Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys  
 450 455 460

agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg 1440  
 Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu  
 465 470 475 480

tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc 1488  
 Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser  
 485 490 495

ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt 1536  
 Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu  
 500 505 510

ctt cat gct ttc aga att cgt gcg gtg acc atc aat aga atg atg tcc 1584  
 Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser  
 515 520 525

tac ttg aac tct tcc 1599  
 Tyr Leu Asn Ser Ser  
 530

<210> 62  
 <211> 533  
 <212> PRT  
 <213> Canis familiaris

<400> 62

Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu  
 1 5 10 15

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val  
 20 25 30

## IM-5

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
 35 40 45  
 Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln  
 50 55 60  
 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
 65 70 75 80  
 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val  
 85 90 95  
 Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
 100 105 110  
 Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
 115 120 125  
 Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
 130 135 140  
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg  
 145 150 155 160  
 Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser  
 165 170 175  
 Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
 180 185 190  
 Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro  
 195 200 205  
 Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
 210 215 220  
 Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr  
 225 230 235 240  
 Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
 245 250 255  
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu

260		265		270
Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp	275	280		285
Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp	290	295	300	
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp	305	310	315	320
Ser Asp Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser	325	330		335
Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu	340	345		350
Asn His Ser Gln Thr Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys	355	360	365	
Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp	370	375	380	
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu	385	390	395	400
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile	405	410		415
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe	420	425		430
Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr	435	440	445	
Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys	450	455	460	
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu	465	470	475	480
Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser	485	490		495

## IM-5

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu  
500 505 510

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser  
515 520 525

Tyr Leu Asn Ser Ser  
530

<210> 63  
<211> 1599  
<212> DNA  
<213> Canis familiaris

<400> 63  
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aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt 120  
ctgtggcaca gtcacactgt tgaaattcag ggctgtaac agctcatcga tagctgtcag 180  
catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240  
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300  
cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360  
ggaagccagg caactctcat tcatggttaa ttccagtggg aagcaggcct ccactgtgct 420  
ggttttatcc tttgtgatat cttcatgac aatctcttcg gaagtgcagg aatataattc 480  
tagagtttgt ctggccttct gaagcgtggt gctgacggct ctcaacaagg tttgggagtg 540  
gttcaaacat tggaacatac ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600  
gccaccgcca ccactgcatg acacagatgc ccagtgcctc caggatgaac tatagtagcg 660  
gtctcgggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720  
gtccacgcag agtctatctt tcttttctct attgttcttg ccttgggcct gtatgcaaaa 780  
tgtcagggag aagtaggaat gtgggggtgct ccagggtgctg gggatttccc agctgacctc 840  
cacgtgccga gaatttttca atggcttcag ctgcaggttt gtgggtgggt ctggtttgat 900  
gatgtctctg atgaagaagc tgctgggtga gttttcatac ttgagcttgt gaatagcatc 960  
caccacgacc tcgatgggta ggctctcctc ggcagagggg caggcactgc cctcctgaca 1020  
ctccactgtg tacttcttat aatccctggt gtccactctg accctctctg ctgaaagtgt 1080  
cactgtcca catgtcacc cttgggggtc agagaagcct ctgctacttt tgacactgaa 1140  
tttcaaataca gtactgattg ccgtcagcca ccagcatgtg aaacgtccag aataattctt 1200  
tgctcacat ttcagaaaga tcttattttt ggattctttc tgttccttta agatatcagt 1260



ggaccaaatt ccattcttctt ttttgtgaat caacaggagt gagcggctca gaaccttgcc 1320  
 tccttttatgg caggtatact ggccagcatc tccaaattct ttgacttgga tggtcagagt 1380  
 tttaccagaa cctaggactt cactgctctg cgctgaggtc caagtgatgt catcttcttc 1440  
 aggggtatgg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500  
 tacaacataa acatctttctt ccagttccca tatggccatg aggggagacg ccagcaaaac 1560  
 gagggaaaac caggagatga ccaactgctg aggggtgcat 1599

<210> 64  
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 <212> DNA  
 <213> Canis familiaris

<400> 64  
 000

<210> 65  
 <211> 0  
 <212> DNA  
 <213> Canis familiaris

<400> 65  
 000

<210> 66  
 <211> 1533  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (1)..(1533)  
 <223>

<400> 66  
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 Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His  
 1 5 10 15

cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa 96  
 Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu  
 20 25 30

gaa gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt 144  
 Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly  
 35 40 45

tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc 192  
 Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly  
 50 55 60

cag tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg 240



Figure 1 consists of 12 histograms arranged in a single column. Each histogram represents the distribution of the number of non-zero elements in the vector  $x$  for a specific value of  $n$ . The x-axis for all histograms is labeled 'Number of non-zero elements' and ranges from 0 to 120. The y-axis is labeled 'Frequency' and ranges from 0 to 100. The histograms are labeled with  $n$  values: 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, and 120. As  $n$  increases, the distribution of non-zero elements shifts to the right, indicating that the vector  $x$  contains more non-zero elements as  $n$  increases.

<400> 67

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Ile	Trp	Glu	Leu	Glu	Lys	Asp	Val	Tyr	Val	Val	Glu	Leu	Asp	Trp	His	1	5	10	15
Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu	Thr	Cys	His	Thr	Pro	Glu	20	25	30	
Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Ala	Gln	Ser	Ser	Glu	Val	Leu	Gly	35	40	45	
Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys	Glu	Phe	Gly	Asp	Ala	Gly	50	55	60	
Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Lys	Val	Leu	Ser	Arg	Ser	Leu	Leu	65	70	75	80
Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	Ser	Thr	Asp	Ile	Leu	Lys	85	90	95	
Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	Leu	Lys	Cys	Glu	Ala	Lys	100	105	110	
Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu	Thr	Ala	Ile	Ser	Thr	115	120	125	
Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg	Gly	Phe	Ser	Asp	Pro	Gln	130	135	140	
Gly	Val	Thr	Cys	Gly	Ala	Val	Thr	Leu	Ser	Ala	Glu	Arg	Val	Arg	Val	145	150	155	160
Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	Glu	Cys	Gln	Glu	Gly	Ser	165	170	175	
Ala	Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Asp	180	185	190	
Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile	195	200	205	
Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	Asn	Leu	Gln	Leu	Lys	Pro	210	215	220	
Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr	225	230	235	240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala  
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys  
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln  
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val  
290 295 300

Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro  
305 310 315 320

Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu  
325 330 335

Leu Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu  
340 345 350

Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys  
355 360 365

Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met  
370 375 380

Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly  
385 390 395 400

Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu  
405 410 415

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala  
420 425 430

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp  
435 440 445

Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe  
450 455 460

Asn Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe

465 470 IM-5 475 480  
 Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile  
                   485                  490                  495

Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser  
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<210> 68  
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 <213> Canis familiaris

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 ctgtggcaca gtcacactgt tgaaattcag ggctgtaac agctcatcga tagctgtcag 180  
 catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240  
 cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300  
 cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360  
 ggaagccagg caactctcat tcatgggttaa ttccagtggg aagcaggcct ccactgtgct 420  
 ggttttatcc tttgtgatat cttcatgatc aatctcttcg gaagtgcagg aatataattc 480  
 tagagtttgt ctggccttct gaagcgtggt gctgacggct ctcaacaagg tttgggagtg 540  
 gttcaaacat tggaacatac ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600  
 gccaccgcca ccactgcatg acacagatgc ccagtcgctc caggatgaac tatagtagcg 660  
 gtctcgggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720  
 gtccacgcag agtctatctt tcttttctct attgttcttg ccttgggcct gtatgcaaaa 780  
 tgtcagggag aagtaggaat gtggggtgct ccaggtgtcg gggattccc agctgacctc 840  
 cacgtgccga gaatttttca atggcttcag ctgcaggttt gtgggtgggt ctggtttgat 900  
 gatgtctctg atgaagaagc tgctgggtga gttttcatac ttgagcttgt gaatagcatc 960  
 caccacgacc tcgatgggta ggctctcctc ggcagagggg caggcactgc cctcctgaca 1020  
 ctccactgtg tacttcttat aatccctggt gtccactctg accctctctg ctgaaagtgt 1080  
 cactgctcca catgtcacc cttgggggtc agagaagcct ctgctacttt tgacactgaa 1140  
 tttcaaataca gtactgattg ccgtcagcca ccagcatgtg aaacgtccag aataattctt 1200  
 tgccctcatat ttcagaaaga tcttattttt ggattctttc tgttccttta agatatcagt 1260

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ggaccaaatt ccattcttctt ttttgtgaat caacaggagt gagcggctca gaaccttgcc	1320
tccttttatgg caggtatact ggccagcatc tccaaattct ttgacttgga tggtcagagt	1380
tttaccagaa cctaggactt cactgctctg cgctgaggtc caagtgatgt catcttcttc	1440
aggggtatgg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc	1500
tacaacataa acattcttctt ccagttccca tat	1533

<210> 69  
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<220>  
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<400> 69	
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<210> 70  
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<210> 72  
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<400> 73  
 aactattgag cacagggata aagatgactg

30

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33

<210> 75  
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36

<210> 76  
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37

<210> 77  
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28



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<210> 80  
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<400> 80  
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<210> 81  
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<400> 81  
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<210> 82  
 <211> 39  
 <212> DNA  
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<220>  
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<400> 82  
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<210> 83  
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 <220>  
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 <400> 83  
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 <210> 84  
 <211> 60  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Synthetic Primer  
  
 <400> 84  
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 <210> 85  
 <211> 28  
 <212> DNA  
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 <400> 85  
 atgcatcctc agcagttggt catgcct 28  
  
 <210> 86  
 <211> 25  
 <212> DNA  
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 <223> Synthetic Primer  
  
 <400> 86  
 tgcaggacac ggatgcccag ttgct 25  
  
 <210> 87  
 <211> 37  
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 <400> 87

acaggtacca tgcatacctca gcagttgggc atcgccct

37

<210> 88  
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<400> 88  
 ctaactgcag gacacggatg cccag

25

<210> 89  
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19

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27

<210> 91  
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39

<210> 92  
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<210> 93  
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<400> 93  
ccatcctggg cctgctaagc 20

<210> 94  
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<220>  
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ccatctggta catcttcaag tc 22

<210> 95  
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<212> DNA  
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aaaaaaccgg ggtatgttcc aatgtttcaa ccactccc 38

<210> 96  
<211> 51  
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<220>  
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<210> 97  
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<400> 97  
cttaaaggaa cagaaagaat cc 22

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<213> Artificial sequence

<220>  
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<400> 98  
ggtattccca gctgacctc 19

<210> 99  
<211> 37  
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<220>  
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<400> 99  
cataggtacc atgcaccctc agcagttggt catctcc 37

<210> 100  
<211> 29  
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<220>  
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<400> 100  
atctaaatgc atgacacaga tgcccagtc 29

<210> 101  
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<212> DNA  
<213> Felis catus

<220>  
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<222> (1)..(561)  
<223>

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Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile  
1 5 10 15

agc aac acg ctt cag aag gcc aga caa act cta gaa ttt tac tcc tgc 96  
Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys

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act	tcc	gaa	gag	att	gat	cat	gaa	gat	atc	aca	aaa	gat	aaa	acc	agc	144
Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp	Lys	Thr	Ser	
	35						40					45				
aca	gtg	gag	gcc	tgc	tta	cca	ctg	gaa	tta	acc	atg	aat	gag	agt	tgc	192
Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Thr	Met	Asn	Glu	Ser	Cys	
	50					55					60					
ctg	gct	tcc	aga	gag	atc	tct	ctg	ata	act	aat	ggg	agt	tgc	ctg	gcc	240
Leu	Ala	Ser	Arg	Glu	Ile	Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala	
65					70				75					80		
tcc	aga	aag	acc	tct	ttt	atg	acg	acc	ctg	tgc	ctt	agc	agt	atc	tat	288
Ser	Arg	Lys	Thr	Ser	Phe	Met	Thr	Thr	Leu	Cys	Leu	Ser	Ser	Ile	Tyr	
			85						90					95		
gag	gac	ttg	aag	atg	tac	cag	gtg	gag	ttc	aag	gcc	atg	aat	gca	aag	336
Glu	Asp	Leu	Lys	Met	Tyr	Gln	Val	Glu	Phe	Lys	Ala	Met	Asn	Ala	Lys	
			100					105					110			
ctg	tta	atg	gat	cct	aaa	agg	cag	atc	ttt	ctg	gat	caa	aac	atg	ctg	384
Leu	Leu	Met	Asp	Pro	Lys	Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu	
		115					120					125				
aca	gct	att	gat	gag	ctg	tta	cag	gcc	ctg	aat	gtc	aac	agt	gtg	act	432
Thr	Ala	Ile	Asp	Glu	Leu	Leu	Gln	Ala	Leu	Asn	Val	Asn	Ser	Val	Thr	
	130					135					140					
gtg	cca	cag	aac	tcc	tcc	ctg	gaa	gaa	ccg	gat	ttt	tat	aaa	act	aaa	480
Val	Pro	Gln	Asn	Ser	Ser	Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys	
145					150				155						160	
atc	aag	ctc	tgc	ata	ctt	ctt	cat	gct	ttc	aga	att	cgt	gca	gtg	acc	528
Ile	Lys	Leu	Cys	Ile	Leu	Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr	
				165					170					175		
atc	aat	aga	atg	atg	agc	tat	ctg	aat	gct	tcc						561
Ile	Asn	Arg	Met	Met	Ser	Tyr	Leu	Asn	Ala	Ser						
			180					185								

&lt;210&gt; 102

&lt;211&gt; 187

&lt;212&gt; PRT

&lt;213&gt; Felis catus

&lt;400&gt; 102

Gly	Met	Phe	Gln	Cys	Leu	Asn	His	Ser	Gln	Thr	Leu	Leu	Arg	Ala	Ile
1				5					10					15	

Ser	Asn	Thr	Leu	Gln	Lys	Ala	Arg	Gln	Thr	Leu	Glu	Phe	Tyr	Ser	Cys
			20					25					30		

Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	Asp	Lys	Thr	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35

40

45

Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser Cys  
50 55 60

Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala  
65 70 75 80

Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr  
85 90 95

Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys  
100 105 110

Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu  
115 120 125

Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn Ser Val Thr  
130 135 140

Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys  
145 150 155 160

Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr  
165 170 175

Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser  
180 185

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<211> 561

<212> DNA

<213> Felis catus

<400> 103

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ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agtcatcaa tagctgtcag 180

catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240

cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300

cataaaagag gtcttttctgg aggccaggca actcccatta gttatcagag agatctctct 360

ggaagccagg caactctcat tcatgggttaa ttccagtggg aagcaggcct cactgtgct 420

## IM-5

ggttttatct tttgtgatat cttcatgac aatctcttcg gaagtgcagg agtaaaattc 480  
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 gttgaggcac tggaacatcc c 561

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 <213> Canis familiaris

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 <222> (232)..(897)  
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 gccattata aaaatgtgac cccccgggtc ggctcccccac cgccgccctc cctgtcccgcg 180  
 tccgcagtcc gcgtccagcg cccgccgggg tccacgcagc gcccgcccag c atg tgc 237  
 Met Cys  
 1  
 ccg ccg cgc ggc ctc ctc ctt gtg acc atc ctg gtc ctg cta agc cac 285  
 Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu Ser His  
 5 10 15  
 ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca ccg agc 333  
 Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser Pro Ser  
 20 25 30  
 cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg aga gcc 381  
 Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu Arg Ala  
 35 40 45 50  
 gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta tat tcc 429  
 Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu Tyr Ser  
 55 60 65  
 tgc act tcc gaa gag att gat cat gaa gat atc aca aag gat aaa acc 477  
 Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr  
 70 75 80  
 agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat gag agt 525  
 Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser  
 85 90 95  
 tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg agt tgc ctg 573  
 Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu  
 100 105 110  
 gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt agc agc atc 621  
 Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser Ser Ile



## IM-5

115	120	125	130	
tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc atg aac gca				669
Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met Asn Ala	135	140	145	
aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat caa aac atg				717
Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met	150	155	160	
ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc aac agt gtg				765
Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn Ser Val	165	170	175	
act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt tat aaa act				813
Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr	180	185	190	
aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt gcg gtg				861
Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val	195	200	210	
acc atc gat aga atg atg agt tat ctg aat tct tcc taaaaagctg				907
Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser	215	220		
agggtctctct cgactttaaa gtcattccta taaaaatgtg aacccaaaag aatttttcat				967
aagatagggg ttaagaacca gggaggggggt ggcttgacct ggtcctactt aagctagtag				1027
gataattctc atgcttggtt acattagttg ccactcaaat tttgaaagat gtgactgtta				1087
tatccacac gatgcctttg accaagtata tttcacattt actatggata agttaagtgt				1147
tcgtgagcaa attgctaaag aggaaaaatg tcctcaccga acatgttttt attttccctt				1207
taatagaaga gcaagacttt ataagctatt tctgtaccaa actgttttga gaaacaaaca				1267
ctcaagcata atttatttaa aaatacttat ttatataatt ttgtgttcat gaaagcatgt				1327
gaattaattt atatttattt atgttatatt tattaaagta tttattatca agtggatttg				1387
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aaaaaaaa				1455

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 <211> 222  
 <212> PRT  
 <213> Canis familiaris

<400> 105

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1 5 10 15

Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser

20

25

30

Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu  
35 40 45

Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu  
50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp  
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn  
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser  
100 105 110

Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser  
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met  
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln  
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn  
165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr  
180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg  
195 200 205

Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser  
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<210> 106

<211> 1455

<212> DNA

<213> Canis familiaris

<400> 106

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IM-5

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attaattcac atgctttcat gaacacaaaa ttatataaat aagtattttt aaataaatta 180  
tgcttgagtg tttgtttcta caaacagttt ggtacagaaa tagcttataa agtcttgctc 240  
ttctattaaa gggaaaataa aaacatgttc ggtgaggaca tttttcctct ttagcaattt 300  
gctcacgaac acttaactta tccatagtaa atgtgaaata tacttggtca aaggcatcgt 360  
gtgggatata acagtcacat ctttcaaaat ttgagtggca actaatgtaa acaagcatga 420  
gaattatcgt actagcttaa gtaggaccag gtcaagccac cccctccctg gttcttaacc 480  
cctatcttat gaaaaattct tttgggttca cttttttata ggaatgactt taaagtcgag 540  
agagacctca gcttttttagg aagaattcag ataactcatc attctatcga tggtcaccgc 600  
acgaattctg aaagcatgaa gaagtatgca gagcttgatt ttagttttat aaaaatccgg 660  
ctcttcaagg gaggatttct gtggcacagt cacactgttg aaattcaggg cctgtaacag 720  
ctcatcgata gctgtcagca tgttttgatc cagaaagatc tgctctttgg gatccattaa 780  
aagctttgcg ttcattggcct tgaattccat ctggtacatc ttcaagtcct catagatgct 840  
gctaaggcac aggaccgtca taaaagaggg ctttccagag gccaggcaac tcccgttagt 900  
tatcaaagag atctctctgg aagccaggca actctcattc atggttaatt ccagtggtaa 960  
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agtgcaggaa tataattcta gagtttgtct ggccttctga agcgtgttgc tgacggctct 1080  
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cccaggggaac cttgcagcct ggccagaagc aag atg cat cct cag cag ttg gtc 174  
Met His Pro Gln Gln Leu Val  
1 5  
atc tcc tgg ttt tcc ctc gtt ttg ctg gcg tct ccc ctc atg gcc ata 222  
Ile Ser Trp Phe Ser Leu Val Leu Leu Ala Ser Pro Leu Met Ala Ile  
10 15 20  
tgg gaa ctg gag aaa gat gtt tat gtt gta gag ttg gac tgg cac cct 270  
Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His Pro  
25 30 35  
gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa gaa 318  
Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu Glu  
40 45 50 55  
gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt tct 366  
Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly Ser  
60 65 70  
ggg aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc cag 414  
Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly Gln  
75 80 85  
tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg ttg 462  
Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu Leu  
90 95 100  
att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag gaa 510  
Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys Glu  
105 110 115  
cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag aat 558  
Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys Asn  
120 125 130 135  
tat tct gga cgt ttc aca tgc tgg tgg ctg acg gca atc agt act gat 606  
Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr Asp  
140 145 150  
ttg aaa ttc agt gtc aaa agt agc aga ggc ttc tct gac ccc caa ggg 654  
Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln Gly  
155 160 165  
gtg aca tgt gga gca gtg aca ctt tca gca gag agg gtc aga gtg gac 702  
Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val Asp  
170 175 180  
aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt gcc 750  
Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser Ala  
185 190 195  
tgc ccc tct gcc gag gag agc cta ccc atc gag gtc gtg gtg gat gct 798

## IM-5

Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Asp	Ala		
200					205					210					215		
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Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile	Arg		
			220						225					230			
gac	atc	atc	aaa	cca	gac	cca	ccc	aca	aac	ctg	cag	ctg	aag	cca	ttg		894
Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	Asn	Leu	Gln	Leu	Lys	Pro	Leu		
			235					240					245				
aaa	aat	tct	cgg	cac	gtg	gag	gtc	agc	tgg	gaa	tac	ccc	gac	acc	tg		942
Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr	Trp		
		250					255					260					
agc	acc	cca	cat	tcc	tac	ttc	tcc	ctg	aca	ttt	tgc	ata	cag	gcc	cag		990
Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Ile	Gln	Ala	Gln		
	265					270					275						
ggc	aag	aac	aat	aga	gaa	aag	aaa	gat	aga	ctc	tgc	gtg	gac	aag	acc		1038
Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Cys	Val	Asp	Lys	Thr		
280					285					290					295		
tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	gcc		1086
Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln	Ala		
			300					305						310			
cga	gac	cgc	tac	tat	agt	tca	tcc	tgg	agc	gac	tgg	gca	tct	gtg	tcc		1134
Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asp	Trp	Ala	Ser	Val	Ser		
		315					320						325				
tgc	agt	taggttccac	ccccaggatg	aatcttggag	ggaaagtgga	agatattatg											1190
Cys	Ser																
caaaatttttc	taaggacaca	ttgaagaggc	tccaaaagtt	attttctgcc	taatttttctt												1250
tttgtaaagg	gtcattattg	tgtcttcgca	atatttttta	catttaaag	ccaaatgccc												1310
actgaaacaa	tcagctactt	tatttataga	ttttcagcta	gcaggctgcc	actgacctta												1370
atgctatttta	aatattttaag	taatttatgt	atattattaat	ttattgttat	tgaacacttg												1430
tgtgccaaga	tatattgtat	gtttcatacc	ctcaggacct	gatctgtaag	gaataggccc												1490
tattatgcaa	aatgtgaatt	tatgtgttat	ttatactgac	aacttttcaa	gcaagaatgt												1550
atcatttttta	tgacaaccag	tgagcacaca	atattatgat	gccagcacca	taatataattt												1610
gtgatggatg	ggaacacaga	ggtagttaaa	tagagacatg	gagacacgaa	tccatttgag												1670
aagtttctgg	agacggagat	gttagatcct	gtatccataa	agacttcctt	gcggtggtgt												1730
tgataaagca	attcagggcc	acttgcattt	ttaagcaagt	ttagtttttg	gatgcctgaa												1790
tttagaaaga	cctgagacaa	ataactcaaa	ttgagattca	gcttcagcca	ccttgccagt												1850
ccccatcccc	atctatctgt	aagtcattgg	agagtgaccc	agggacactg	taagtgtctg												1910

## IM-5

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tgggtcaagaa ttgcttactg gacagcgcaa gtgaacctga ctgggtggatg tgaccagaaa 2090  
gtgccaatcg ctgaggtgct acttttaagt aatgaatgtg ctttctgtaa agtgatttca 2150  
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tcttgtttgc aataataaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 2267

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<400> 108

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Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln  
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val  
85 90 95

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
100 105 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg  
145 150 155 160

IM-5

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser  
165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro  
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr  
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
260 265 270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp  
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
305 310 315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser  
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<210> 109

<211> 2267

<212> DNA

<213> Canis familiaris

<400> 109

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aatcacttta cagaaagcac attcattact taaaagtagc acctcagcga ttggcacttt 180

ctggtcacat ccaccagtca ggttcacttg cgctgtccag taagcaattc ttgaccattt 240

Variable	Mean		SD		t		p	
	Control	Case	Control	Case	Control	Case	Control	Case
Age	30.5	30.5	1.2	1.2	0.0	0.0	0.999	0.999
Gender	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Education	12.0	12.0	1.0	1.0	0.0	0.0	0.999	0.999
Income	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Marital status	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Occupation	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Religion	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Health status	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Family size	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Urban/rural	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Time of day	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Season	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Weather	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Time of day	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Season	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Weather	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Time of day	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Season	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Weather	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Time of day	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Season	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Weather	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Time of day	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Season	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Weather	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Time of day	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Season	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Weather	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Time of day	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Season	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Weather	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Time of day	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Season	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Weather	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Time of day	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Season	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Weather	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Time of day	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Season	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Weather	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Time of day	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Season	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Weather	1.0	1.0	0.0	0.0	0.0	0.0	0.999	0.999
Time of day	1.0	1.0	0.0	0.0	0.0			

—



IM-5

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ctcctgctgc	tgtgtctact	gctactggag	cttatatacc	ctactcctac	cgagcttttg	2220
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